

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Gatanaga, Tetsuya
Granger, Gale A.

(ii) TITLE OF INVENTION: Factors Altering Tumor Necrosis Factor Receptor Releasing Enzyme Activity.

(iii) NUMBER OF SEQUENCES: 154

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: BOZICEVIC, FIELD, & FRANCIS, LLP
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(C) CITY: Menlo Park
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94025

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: Windows
(D) SOFTWARE: FastSEQ for Windows Version 2.0b

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/700,354
(B) FILING DATE: 13-NOV-2000
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/081,385
(B) FILING DATE: 14-MAY-1998

(A) APPLICATION NUMBER: PCT/US99/10793
(B) FILING DATE: 14-MAY-1999

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Francis, Carol L.
(B) REGISTRATION NUMBER: 36,513
(C) REFERENCE/DOCKET NUMBER: IRVN-007CIP2

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-327-3400
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(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4047 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAGCTTTTG	CTTCCCTTCC	CCGGGAAAGG	CCGGGGCCAG	AGACCCGCAC	TCGGACCAGG	60
CGGGGGCTGC	GGGGCCAGAG	TGGGCTGGGG	AGGGCTGGGA	GGCGCTCTGG	GGCCGGCTCC	120
TCCAGGCTGG	GGGCCGCCAG	CTCCGGGAAG	GCAGTCCTGG	CCTGC GGATG	GGGCCGCCGCG	180
TGGGGCCCGG	GGGGCGGCC	TCGGGAGGCG	TCCAGGCTGC	GGGAGC GGGGA	GGAGC GGGCCG	240
TGCGGGCGCC	AGCGCCGTGG	GTGGAGGTG	CCGTCCCTCC	TGAGGGGCAG	CCAGTGC GTT	300
TGGGACCCGG	GAGCAGAGCC	CGCGCCTCCC	CAGCGGCCTC	CCC GGGGTC	TCACCGGGTC	360
ACCCGAGAGC	GGAGGCCCCG	GCTCCGCAGA	AACCCGGGGC	GGCCGCGGGG	AAGCAGCGCC	420
CTCAGGCGTC	GGAGGAGCCC	CCAGAAGGAC	CTCGCGCCTT	CCC GCGGGC	TCCGACCGCC	480
TGGGTTCGGT	GCGGGACGGC	CCAGGCCGCC	AGGACCCCCA	AGCGCAGCTC	AGTCTGC GGGG	540
GCACGACCCA	GAGGCCAGCA	GCAGAGGACG	GGGCCGGGGC	CGGGAGAGGG	CGGGGAGGGC	600
GCTCCTGGGA	GGTCAAGGCC	AGGGCTAGAC	TTTCAGGGTC	ATGGCCTGGC	CCCTCATCCC	660
CAGGGAGGTG	AGGGGGCTCT	GTGAGCAGAG	GGGGCCCGG	TGGAGAAGGC	GCTGCTAGCC	720
AGGGGGGGGG	CAGGAGCCCA	GGTGGGGACT	TAAGGGTGGC	TGAAGGGACC	CTCAGGCTGC	780
AGGGATAGGG	AGGGAAAGCTA	GGGGTGTGGC	TTGGGGAGGT	GCTGGGGAC	CGCGGGCGCC	840
CTTTATTCTG	AAGCCGAATG	TGCTGCCGGA	GTCCCCAGTG	ACCTAGAAAT	CCATTCAAG	900
ATTTTCAGGA	TTTCAGGTG	GAGACAAAGG	CCAGGCCAG	GTGAAAATGT	GGCA GTGACA	960
GAGTATGGGG	TGAGAACACAC	GGAGAGAGGA	AGTCCCCGAG	GCGGATGATG	GGACAGAGAG	1020
CGGGGACCA	AATTTTTAA	AACGCATCTG	AGATGC GTTT	GGCAGACTCA	TAGTTGTTT	1080
CCTTTCACGG	AGAAAAGTGTG	GGCAGAAGCC	AGCTCTAAAG	CCCAGGCTGC	CCAGCCTGCA	1140
CTGGCAGAGC	TGACGGAAGG	CCAGGGCAGA	GCCTCCCTC	CCTGTCACAG	ACATGAGCCC	1200
TGGAGATCTG	GAATGAGGCA	GATGTGCCCA	GGGAAAGCTG	ATCCGCCCG	ACCCAGGGCC	1260
CCCCGGGTGC	CCCTTGAGC	GTGGAATCGT	TGCCAGGTCA	TGGCTCCCTG	CTATCGAAC	1320
CCGGACACGG	GTCGTGTGCT	GCACCTGGCA	GTTGCAGGAC	CGACACCCAC	AATGCCTTAA	1380
GAGGTGATGA	CTGCCCTCCA	GGGGCCTGGC	TGGCTGACAC	TTTGCATGGC	TCCTGGAGAA	1440
GAGGGATTGA	GTGGAGTCCA	CGGGTCATGG	CCACGCTCTG	GGT GCTGCC	CTGAGGCAGG	1500
GCCCCGGCTGG	GGTGAGAAGG	GGCTGGAGAC	AGGTTCTGC	CAGTTCAGCC	TCTAACCGGT	1560
GGTCTTCATG	CCTAGGAACC	CACTGGGGC	TTATGAAACT	GCAGGTGGCT	GAGTCTTGC	1620
CATGGGGTCT	CTCCTCAGG	AGGTCTGGGT	GGGGCCGGAG	ACTGTACCCC	ACAAAGGGTC	1680
CCAGGTGAGG	CGGATGTGGC	CTGGCGCTGT	GTGGCTCTGG	ACCTAGTCCT	TGGGCTTGGG	1740
CTGGCGCCCA	GGGCCTGGGC	TTGAGACAGC	TGTGACGCAG	GCAAGCCATT	TACCCCGTTT	1800
GTGGGGACAT	TACATCTTCC	TAGCTTGGAA	CACACAGGA	GCCAGGGTTG	TTATCCACAT	1860
TCCTCCTCCA	TGTTCTTCTC	TTGAGAACCT	TTACCA GGT	TGTCAGGAGC	TGGGCTCCAC	1920
CAGGGAGACT	CAAGTGGAAA	GCCCTCATCC	TTGTCCTCCA	GGAGACAGGA	AAACCTATGG	1980
TTACAATTCC	AGGGACAAGA	GGCATGCATG	TGAGGTGTGG	CAAATCTCAC	TGTTCAACTG	2040
GAGAAATCAG	AGACAGCTTC	CTGGAGGCA	TGACACCTGG	ACAGGCTCT	CCACAGGAGG	2100
AAGCGAGTGA	GAGAAGCCAA	CTGGGATGGA	CCCATCATGT	AGGGGGAAACA	GTGCGCGCAG	2160
AACCAACAAAC	CACCCCCACC	CTAGGCCAG	AGCTCACGGA	GAGAGCTGGG	CCTCTCGGGG	2220
TGACTACATA	GTTCCTGCT	GGATCTTAGG	TCTTGTCTT	GGGCAGCTCT	GCTGAGACCT	2280
CTATGCCTGT	TCCAGGCTGC	ACCAAGGTT	TGTGACTATT	GGTCTGGGGT	TGTTTGCA	2340
CAACTGAAGT	GTTCTGTTGT	AAAACAGGCA	CTTGATTTC	TGGAAGGAAT	GCTGTTGTT	2400
CTTGCTGCGA	CAAACATTGA	GCAGCATTTA	GTGGGCGGTT	TATATCTGT	GGAGTAATGG	2460
GTGTTTTGA	AGTCTGTCT	GGGTACTGCA	CATTAAGG	AATATCATT	TCTGAAACAT	2520
TGCTATTTTC	CACACCAGAA	ATCATATCT	CTTGTGGTC	CATGTCTGAA	GACCTTACAC	2580
GAGAAAGTCT	TAATGTAAGT	TTAGTAGAGT	CCTTGGATGG	AGAACTAATT	ATATCATA	2640
TTGCCGCTTT	CTCACTCTGC	TCTTTTCAT	CCTTGCCTAA	TTTCATTTC	TTCTGCTTCT	2700
TTTGTGTTCT	TTCTGGAGAA	TCTAGCAAGA	TATCTGGTGG	AAACATCTCGA	GGTGATGAAC	2760
AAGGTAGAGA	CTGAGATTGT	AGGATTAAGG	GTGGCTTGA	GCCTTTAGGA	GTTCCTTCAC	2820
TTCCAGCAGG	GGAGCATACT	GGCTGTGGAG	ATCTCAAGGG	AAAAGATGCA	GCATTCCCTCA	2880
TTGTTGAAGA	ATCTCCATCG	TCACTACTTA	GCCTGTGCAC	CATGTGTAGG	TAGTCCTCAC	2940
TTGAACCATG	TCTAGGATTA	TCAGCATGAT	GATTAGCTGA	ATTGCCAGAC	AACGGACAG	3000

AAACTTTATT	ATCATGTATG	TTTCTCAAAC	CACCTGCAAC	AATGGGACTT	GATACCGATG	3060	
CTTGTGCA	CTGTGGATGT	GTTGTGAA	CTGAAGGATG	GGAATATGGC	ATGTATCCTG	3120	
CAGGGCTTG	TGGGGCGTAT	GGACTAGGCA	CTGGGCTATT	TTGCTGTGGC	ATAAAATCTGT	3180	
TCCCCAGAGCT	TGTCTGTGGT	GGCACAAACC	GGCTGGAGGG	GCTATGTGAG	ATAGTGGTTT	3240	
GTTGATAATT	GGAAAGATGCA	GGACTACTGT	GCATGGAATT	CTGAGAAAGT	TTATACTGAG	3300	
ACATCATCAT	TCCACTTTGT	ACATATCTGT	TCTGCATGCT	TTTCTCCCTG	AAAACATTAG	3360	
GA	ACTCCTTGC	CAGGACGGCC	TGCAACAAAGA	CTGGTATGTC	ACCTTCTGGG	TCATCACTGC	3420
CAAGGTTATC	TTTCAACTCT	ATGTGATCTG	TTGATACCTG	GTTGAGGCTA	TGGACAAGCT	3480	
GTGAAACCAA	ATTGTCATCC	CTACAAGCCA	AAAGGCAGTT	CACCTCTTCT	GCTATTCTG	3540	
CATTAAAGAG	AAGGCTCTT	GTAGTTGTAG	CAGGTAAGG	AGATGGAAGA	GGCAGCTGGT	3600	
TCAGGAGGTC	TGTGAGACTA	GCAATCCCCG	CAAGAGTAGT	AATGGGGACA	TGGGGCATAT	3660	
CCCCATTCA	CCTGAATTTC	TGGAATGGTG	TTGCCTATAA	AAGTACTTAG	TTCAGGTGCC	3720	
AGCTGTCATT	ACTTCCCATT	TCCCAAACAC	TGGGCAGAATC	GGCGTCTGAA	TCCAAGGGGA	3780	
GGCCGAGGCC	GCTGTGGCGA	GAGACTATAA	TCCGGGCCGG	GAGGGGGGGC	GGCTACGGCT	3840	
CCTCTTCCGT	CTCCTCAGTG	CGGGGAACAT	GTAGAGCCGG	GGGGAGACCA	GCCGAGAAGA	3900	
CAAATCGTT	CTTCTTCTTC	CTCCTCCTCC	TCCTCTCCC	ACATAGAAAC	ACTCACAAAC	3960	
ACCCGACCAC	GGGCCCGAGC	TACCGGGGGG	GCATCGCCGC	GGGCCGGGA	ACCAATTCTC	4020	
CTGTCGGCGG	GGCGTCCTT	TGGATCC				4047	

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 739 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGATCCAAAG	GTCAAACCTCC	CCACCTGGCA	CTGTCCCCGG	AGCGGGTCGC	GCCCAGGCCGG	60
CGCGCGGCCG	GGCGCTTGGC	GCCAGAACG	AGAGCCCCTC	GGGGCTCGCC	CCCCCGCCTC	120
ACCGGGTCAG	TGAAAAAAACG	ATCAGAGTAG	TGGTATTTC	CCGGCGGCC	GCAGGGCCGG	180
CGGACCCCGC	CCCAGGGCCCC	TCGGGGGAC	ACCGGGGGGG	CGCCGGGGGC	CTCCCACTTA	240
TTCTACACCT	CTCATGTCTC	TTCACCGTGC	CAGACTAGAG	TCAAGCTCAA	CAGGGTCTTC	300
TTTCCCGCT	GATTCCGCCA	AGCCCGTTCC	CTTGGCTGTG	GTTCGCTGG	ATAGTAGGTA	360
GGGACAGTGG	GAATCTCGTT	CATCCATTCA	TGCGCGTCAC	TAATTAGATG	ACGAGGCATT	420
TGGCTACCTT	AAGAGAGTCA	TAGTTACTCC	CGCCGTTTAC	CCGCGCTTCA	TTGAATTCT	480
TCACCTTGAC	ATTCAGAGCA	CTGGGCAGAA	ATCACATCGC	GTCAACACCC	GCCGCGGGCC	540
TTCGCGATGC	TTTGTTTAA	TTAACACAGTC	GGATTCCCCT	GGTCCGACCC	AGTTCTAAGT	600
CGGCTGCTAG	GCGCCGGCCG	AAGCGAGGCG	CCGCGCGAA	CCGCGGCC	CGGGGCGGAC	660
- CCGCGGGGGG	GACCGGGCCG	CGGCCCCCTCC	GCCGCCCTGCC	GCCGCCGCC	CCGCCGCGCG	720
CCGAAGAAGA	AGGGGGAAA					739

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 233 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAAGAGTGGC GGCGCAGCA GGCCCCCGG GTGCCGGGC CCCCCTCGAG GGGGACAGTG	60
CCCCCGCCGC GGGGGCCCCG CGGGGGCCCG CGGCCGCCCG CTGCCGCCGC GACCCTTCTC	120
CCCCCGCCGC CGCCCCCACG CGGGCCTCCC CGGGGGAGGG GGGAGGACGG GGAGCAGGGGG	180
AGAGAGAGAG AGAGAGAGGG CGCGGGGTGG CTCGTGCCGA ATTCAAAAG CTT	233

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGATCCAAAG AATTCCGCAC GAGGTAGTCA CGGCTTTGT CATTGTTGTA CTTGACGTTG	60
AGGCTGGTGA GCTTGGAAAA GTCGATGCGC AGCGTGCAGC AGGCGTTGTA GATGTTCTGC	120
CCGTCCAGCG ACAGCTTGGC GTGCTGGCG CTCACGGGT CGCGATACTG CAGCAGGGCC	180
TGGAACTGGT TGTTCTTGGT GAAGGTGATG ATCTTCAACA CTGTGCCGAA CTTGGAGAAA	240
ATCTGGTGCAC GCACATCCAG GGTACACAGGG TAGAAGAGGT TCTCCACGAT GATCCTGAGC	300
ACGGGGCTCT GCCCCGCCAT CGCCATCCCT GCATCCACGG CGGCCGCCGA GGCAGCCAAG	360
GCCAGGTTCC CCGACTGGAC CGAGTTCACC GCCTGCAGGG CGCCTGGC CCGCGCCTGG	420
TTGGGAGAGC TGTCGGTCTT CAGCTCCTG TGGTTGGAGA ACTGGATGTA GATGGGCTGG	480
CCGCGCAGCA CAGGGGTCAC CGAGGTGAG TAGTTCACCA TGGTATTGGC AGCCTCCTCC	540
GTGTTCATCT CGATGAAGGC CTGGTTTTTC CCCTCAGCA TCAGGAGGTT GGTGACCTTC	600
CCAAAGGGCA GCCCCAGGGG GATGACTTCC CCCTCCGTGA CGTCGATGGG GAGCTCCGG	660
ATGTGGATCA CTCTAGAGGG GACGCCGTCA CTTCCGGCTGT CACCTTGAA CTTCTTGCTG	720
TCATTTCCGT TTGCTGCAGA AGCCGAGTTG CTGCTCATGA TAAACGGTCC GTTAGTGACA	780
CAAGTAGAGA AAAGCTCGTC AGATCCCCGC TTTGTACCAA CGGCTATATC TGGGACAATG	840
CCGTCCATGG CACACAGAGC AGACCCGGGG GGGACGGAGT GGAGGCGCCG GAATCCTGGA	900
GCTAGAGCTG CAGATTGAGT TGCTGCAGA GACGAAGCGC AAGTATGAGA GTGTCCTGCA	960
GCTGGGCCGG GCACGTGACAG CCCACCTCTA CAGCCTGCTG CAGACCCAGC ATGCACTGGG	1020
TGATGCCTTT GCTGACCTCA GCCAGAAGTC CCCAGAGCTT CAGGAGGAAT TTGGCTACAA	1080
TGCAGAGACA CAGAAACTAC TATGCAAGAA TGGGGAAACG CTGCTAGGAG CCGTGAACCTT	1140
CTTTGTCTCT AGCATCAACA CATTGGTCAC CAAGACCATG GAAGACACGC TCATGACTGT	1200
GAAACAGTAT GAGGCTGCCA GGCTGGAATA TGATGCCTAC CGAACAGACT TAGAGGAGCT	1260
GAGTCTAGGC CCCCAGGGATG CAGGGACACG TGGTCGACTT GAGAGTGCCTT AGGCCACTTT	1320
CCAGGCCCAT CGGGACAAGT ATGAGAAGCT GCGGGGAGAT GTGCCATCA AGCTCAAGTT	1380
CCTGGAAGAA AACAAAGATCA AGGTGATGCA CAAGCAGCTG CTGCTCTTCC ACAATGCTGT	1440
GTCCGCCTAC TTTGCTGGGA ACCAGAAACA GCTGGAGCAG ACCCTGCAGC AGTTCAACAT	1500
CAAGCTGCCG CCTCCAGGAG CTGAGAAACC CTCCGGCTA GAGGAGCAGT GAGCTGCTCC	1560
CAGCCCAACT TGGCTATCAA GAAAGACATT GGGAAAGGGCA GCCCCAGGGT GTGGGAGATT	1620
GGACATGGTA CATCCTTTGT CACTGCCCT CTGGCTTGGG CTCTTTTC TGGCTGGGGC	1680
CTGACACCAAG TTTGCCCCAC ATTGCTATGG TGGGAAGAGG GCCTGGAGGC CCAGAAGTTG	1740
CTGCCCTGTC TATCTCCTG GCCACAGGGC TTCATCCCCA GATCTTTCC TTCCACTTCA	1800
CAGCCAACGG CTATGACAAA ACCACTCCCT GGCCAATGGC ATCACTCTTC AGGCTGGGGT	1860
GTGCTCCCTG ACCAATGACA GAGCCTGAAA ATGCCCTGTC AGCCAATGGC AGCTCTCTC	1920
GGACTCCCTT GGGCCAATGA TGTTGCGTCT AATACCTTT GTCTCTCTC TATGCGTGCC	1980
CATTGCAAGAG AAGGGGACTG GGACCAAAGG GGTGGGGATA ATGGGGAGCC CCATTGCTGG	2040
CCTTGCATCT GAATAGGCCT ACCCTCACCA TTTATTCACT AATACATTTT ATTTGTGTT	2100
TCTAATTAA AATTACCTT TCATCTGCT TGATTTCTC TCAGCTAAAT TAGAAATTG	2160
TAGTTTTCC CCTAAAAAAT TCAATGGCAT TCTTCTTAAATTACATT CTCTGATTTT	2220
CTTGTCAAGC TGCTTCAAGG AAATCCATGT GTTCAAAATG CTTGCTCGCA GTTGTCTCCA	2280
TACCAAATGG TTGCTTAACC CAAATATCTG AGCAGCAAAT TGAGCTGATC CTTCTGGAGA	2340
AAGTACGGTT GAACAGCCAA GACCACTGGG TAGTCGAAGA GAAGACCACA CATCCTGAAC	2400

TCCCCAGTCT	GGTGTGAGGG	GAGGACAGCT	GATAACTGGA	TATGCAGTGT	TCCCAGACAT	2460
CACTGGTCCC	AAACCATTAC	TTCTGCCTGC	CACTGCCACA	AATAACAGTAG	GAATGCCATC	2520
CCCTTCATAC	TCAGCTTAA	TCCTCAGAGT	TTCATCTGGT	CCTTTATGCG	CAGATGTTAC	2580
TCGAAGTTCA	CATGGAATGC	CAAATTTCC	ACAGGCCCTTC	TTGATTTTT	CACAGTGCAC	2640
AAGATCAGAA	GTAGAGCCC	TCAACACTAC	AACCCTGCAC	TGACTTCTG	ATTCAAAAG	2700
CAACTCTACT	CTCTCTGAA	CCCACTAAA	GTTTTCTTT	ACCATTGGA	GCCCTTCAGG	2760
AGTTACTTCT	TTGAGGTCCC	GATAAGACTG	TTTGTCTTC	TGTTGGCTTC	GATCTCCTGA	2820
TGGCCAGAGT	CTCCAGGAAT	CATTGTCAAT	AACATCAGCA	AGAACAAATT	CTTTGGTGGT	2880
TACATCAACA	CCAAATTCAA	TCTTCATATC	AACCAGTGT	CAATTCTGGG	GCAACCAGGA	2940
TTTCTCCAGT	ATTCAAATA	TAGCCTGT	AGCATCTCGT	GCCGAATTCA	AAAAGCTT	2998

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AAGCTTTTG	TGAAAACCT	AGGATATGTC	CCCTCCCTCA	CCACACCCAA	CCCCCGGCC	60
CTGCCCGAGG	ACATGACGAT	GCCTCACACA	CACACACACA	CACACATACA	CACAAGGCCG	120
TGAGCTGCAC	GCAGGAACAT	GGGCTGCACT	CACGACAACA	TTGAAAAAAT	ATACATTATA	180
TATGTACACC	CGGGGGCCCC	ACGTCCCCTC	CCGTCCCCGC	AGCCTGGCCA	CACCAGGTCA	240
CGGAGGAGGG	GCCGGGGCTG	CAGGACCTCA	GGACTGCAAG	GGCAGGAAGG	GAAACAGGAC	300
AAGAAAGGAA	GGAAGTTGGA	AAGGAGGGAG	AAATGGGGTC	CCCAGACTGA	AATGGAAATG	360
AGGTGGGGCG	ATCATAAGAG	AAGCAGGGAC	GATGGTCCAG	CTGAGGGAGC	CCTGCAGAGG	420
GGGAAAGCT	TCCCATGGAC	AGGAGAGAGA	AGGAAGGGG	AGAGGAGAGG	GTTCCTTCA	480
ATCCCACCCC	CAGCCCCAGC	CCCAGCCCCA	GCCATTGCAA	TCGTCACCC	CTCCCCAACAA	540
CAGTGAGTGC	TAAGGGGGCA	GCTGCCATTG	GGGGTAGAAA	GGCAGCTGAA	GTCCAGGCCA	600
CTTTCCAACC	CAGCCAGCCC	CAGTCAAGG	GGCACACCA	GAGCATGACA	GCCCAGAAAGT	660
GAGGGATGGG	GGGCCGGGGG	AGGGCAGGG	CGGACTCCAG	AGGGCCCGCT	GGGGTTTTGA	720
AATGAAAGGA	GGACTGGTTC	TGAAGCCTCT	CTCCCTCTTG	GTCTCTGTGT	TCCCAGAAAG	780
TCCCTCTCCC	ATGTCTGGAG	TGTCTGTTTC	ACCAGGGCAG	AATTCCCCCT	CTGCGTGGGG	840
AGAGGTGTAG	GCCTTAGTAG	CGGTGTGGGG	GGGTCTCGAT	GATGCGTCTC	TCGTCGCTGC	900
TGGGGGAATC	GGCCACCTCC	GAGTCACTGC	TGTCCTCATC	CTCCTGCTGG	CCCCAACAG	960
CCCCCGTCAC	ACAGGACTGC	CGATTCTGGT	AGGACTCCAT	GGGGTTCA	ATGATGGTGA	1020
GAGCTGAGTC	ATCCCAGAAG	AGGTCTGGGT	CCTTGGGGTC	ACTGGAGGCC	CCTGGAGGCC	1080
CGCCGGCCCC	TGAGACGC	CGGTGAAGGG	AATGGATGCG	CACCA	AGGACGACCA	1140
- TGAGCACCAG	GAAGCCCACG	CACACCACAA	TGATGAGGGT	TGCGGCCTG	GGTATCATGG	1200
AGTTTCTGTG	GGAGCTGGCT	AGGCTGTGTC	CAGCCATCTC	AGGCGGGGGC	TGGTGACCAC	1260
GGTGCAGGAA	CTGCTGGGAG	CTGAGCACGT	GGCTGGGGTG	GGCAACCCGG	TTCATGCTGT	1320
GCAGGACATT	GACCTCCACG	ATGAATTCAT	TGCTGGAGTA	ACGGCCATT	ATTCCGAGC	1380
AGGAAAGCCG	GAACCTCCTG	GTGTAGAGGG	CAGCTCCGTG	TCGCAGCCGA	TAACGAGCCT	1440
GCCTCAGGAT	CTCTTCATAC	ACAGTGATGC	TCTCCACCC	AGCAATAGT	AGGTAGGCAG	1500
ATGTGTTGGT	GAGCTCCAGC	CCCCGCTGCT	GCAGAGAGGT	TGTGTCCAGG	AGCAGGCTTT	1560
CCCGCTCGGG	ATCCAGGTCA	TCCCCCACCA	GAGAAATTTC	ACAGCCATCC	AGGTGTC	1620
CAATCTCATC	CGACATGCGT	GTGTCTGTCA	CTGTGCCCTG	CCAAC	TCTTTTTGG	1680
CCTCCACCTG	GTGAGAAATG	GAGCAGGTGA	TTTGAAGATC	AGGAAACAA	GGGACGCCGT	1740
TGGTTCCCTC	AAAGTCCACA	GCTGGCGGG	CAAATGAGC	AGTGCAC	AGCAGGATCT	1800
GGGGGGCGTC	AGGCTGAAGG	ACGACCACGT	AGCCCTCCAC	TTCAGGGATG	GAGACGCAGG	1860
ACTCTTCGCT	GAAGCACTTG	ACAGCAGTGG	TGAGGCGCAG	GGGCCTGACG	CCGGGCGTGG	1920
CAAAGCGCAG	AGTGTTCATG	TAAGCCACAT	GCTGCAGGGC	ATGGTTGAAG	GTCTCCACAT	1980
CATCCCCCTC	CAGGGTGAGC	AGGGACTGTG	AGGGGTTCA	GTGGACCTTC	ATGCCTTTGC	2040

CCAGGCTCTC	GAAATCCCTA	TAGTCCAGCC	CCTCCCGACA	TGCATAGAGG	CACTCGATGA	2100
CCTCGCGCT	CTCCAGCGA	CCTGAGCGCA	CGCTGAAACC	AGCCAGGTAG	CCATGGAAGT	2160
AGTGGTGGAT	CGACAAAGGG	TCTCCTGGG	TGGTGTCTGT	ACTGTTGTCT	CCCTTTCCCT	2220
TCTCTTGTG	CTTCTCCTCA	GTCCAGCAGG	CCCCAATCAT	GAGAGCAGGC	TCCCTTCGGG	2280
GTGGGTGGAT	GAGGCCATTG	TCATGGATGA	GGGCAGGGTC	GAAGGAGATG	CCGTCGGTAT	2340
AGAGTGTGAC	TGTGGGAAAC	TCGAGGTTCA	GAGCGTAGTG	GTGCCACTCA	TCATCACAGA	2400
CCTGCTCCAG	CTTCCAGAGG	AACTTGACTG	GGCAGGGCACT	CTCAAGCAGG	GGCCAGTAGA	2460
GGAAGGCAAT	CCTACAGCCG	TGGACAGTCA	GCGAGTAGTG	AGAGAAGCCG	TCCTCATTCT	2520
GGACAGTGTG	ACATACGATG	GTTCCTCTT	CCTTCTTGCC	CTTGTGGGA	GTACGCCAT	2580
GCTTCATCCA	GAAGGACAGG	GTGAAGTGGT	CACTGAGGCT	GTCCTGGGC	CCAGAGCCCA	2640
GCCCCACTGGG	GCCACCCAGG	GGCACCTGCA	CAGCCTGGGT	GCCATTGAAC	CAGTAGATCA	2700
GGCTGCTGTC	CTGGCTGTAG	TGCACCGAGA	GTCCTGCTGT	CCAGTTGGCA	TTGGGGCCAG	2760
GCATGGGCAA	CAGATCCACT	TCCCCAGTGG	CAGCACCACA	GAGTTCCGC	AGCGCCCGCT	2820
CTGAGTAGTT	GTCACGGTCA	CAGCCCTTGG	CCACATGGCT	GGTCTGCAGC	TCTATGGTGG	2880
CCTGAATGTT	CCAGAGTGGT	TCATCACAGG	TCTCCAGGCG	GATACCAGGG	AACAAAGCCA	2940
AGCTCCCAGC	ACCTGGTGCA	TATTCGATCC	TTTGTTCGA	GCCTTGCAG	CTGGGTTTAC	3000
AGGTGGGCTT	CACCTGAATC	TCCACCTCAG	CATCATCTGC	TGCCCCTTC	TTCCCACAGT	3060
CATAAGCTGT	CACTGTAAAC	TTATAGAGCC	TCTCACCACT	GTACTGCAGC	TTCTCTGTGT	3120
TCTCAATGTT	CCCGTCATTG	TCAATGAGGA	AAGGGGTGTT	GGGTGTGAGA	ATCTCATAGT	3180
AGCAGATCTG	GCTGTACTGG	GGGGAGCAGT	CACCGTCAAT	GGCTTCCACC	CGCAGGATGC	3240
GATCGTACAG	CTTCCCCTCT	GTCACAGCCG	CACGATACAG	CCGTTCCACA	AAACACTGGGG	3300
CAAACCTCGT	CACATCGTTG	ACCCGCACAT	GCACAGTGGC	CTTGTGGGAC	TTCTTGGTGT	3360
TGGCCCGTGC	GGGGCCCTCG	CCACAGTCAT	AGGCCTGGAT	GGTGAAGGTG	TGTTCCCTCT	3420
GGGCCTCGCA	GTCCACAGGC	TCCTTGGCCC	GGATCAGCCC	CTCTCCTGTC	GCCTTGTCAA	3480
GGATCACAGC	CTCAAAGGGC	ACCCCAGACC	CATGGAGCCG	GAAGCCGCAG	ATCTCACCTG	3540
CATAGCGCAG	CGGGGCATCC	TTGTCCAAGG	CAAAGAGTGG	TGGATTCACT	AGGACCGTGT	3600
TGTCATTCTC	CATGACGATG	CCCTGGTACT	CTGCCTCAAT	CCATGGCTTG	TGCTTGTGTTG	3660
CTTTGTTACA	GGAGCAGGAC	GCGAGCAGAG	AGGCCAGCAG	AAGGGGCAGC	AGCAGGAGGG	3720
TCATGGTGC	CGCTGGGGCA	GGGCAGGGCC	AGGCCTTTC	CTCCCCTGGG	AGCCTCCAGC	3780
CTGCGGATT	CACCTGCGG	GAGGGATACA	GGGGGGGAAA	ACCAAAATAA	AACGTCAAAT	3840
AAATTGTGTA	GGAGGAGTCC	AGCTTAGGAC	CGGGCCAGAG	CCAGGCCAGG	CTCGGGGAGG	3900
GGGCCTCTGC	AGGTCAGAG	GATCACTGCT	GCCACCACCG	CCACCCCTGGG	AGCCAGTTAT	3960
TTTGCCATGG	CCTTGATTGC	AACAGCTGCC	TCCTCTGTCA	TGGCAGACAG	CACCGTGTATC	4020
AGGATCTCTT	CTCCACAGTC	GTACTTCTGC	TCAATCTCCT	TGCCAAGGTC	TCCCTCAGGG	4080
AGACGAAGGT	CCTCTCGTAC	CTCCCCGCTG	TCCTGGAGCA	GTGATAGGTA	CCCATCCTGG	4140
ATCTTTGGAT	CC					4152

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGATCCAAAG	ATTCGGCACG	AGTGGCCACA	TCATGAACCT	CCAGGCCAG	CCCAAGGCTC	60
AGAACAAAGCG	GAAGCGTTGC	CTCTTGGGG	GCCAGGAACC	AGCTCCCAAG	GAGCAGCCCC	120
CTCCCCTGCA	GCCCCCCCAG	CAGTCCATCA	GAGTGAAGGA	GGAGCAGTAC	CTCGGGCACG	180
AGGGTCCAGG	AGGGGCAGTC	TCCACCTCTC	AGCCTGTGGA	ACTGCCCT	CCTAGCAGCC	240
TGGCCCTGCT	GAACCTGTG	GTGTATGGGC	CTGAGCGGAC	CTCAGCAGCC	ATGCTGTCCC	300
AGCAGGTGGC	CTCAGTAAAG	TGGCCAAC	CTGTGATGGC	TCCAGGGCGG	GGCCCGGAGC	360
GTGGAGGAGG	TGGGGGTGTC	AGTGACAGCA	GCTGGCAGCA	GCAGCCAGGC	CAGCCTCCAC	420
CCCATTCAAC	ATGGAAC	TGAC	CCAGTCTGT	TGCAACCAAG	GGGAGCCCGC	480

ATCCTGGAGT	GGGAGTCCCG	ACTTACTATA	ACCACCTGA	GGCACTGAAG	CGGGAGAAAG	540
CGGGGGGCC	ACAGCTGGAC	CGCTATGTGC	GACCAATGAT	GCCACAGAAG	GTGCAGCTGG	600
AGGTAGGGCG	GCCCCAGGCA	CCCCTGAATT	CTTCCACGC	AGCCAAGAAA	CCCCCAAACC	660
AGTCACTGCC	CCTGCAACCC	TTCCAGCTGG	CATTGGCCA	CCAGGTGAAC	CGGCAGGTCT	720
TCCGGCAGGG	CCCACCGCCC	CCAAACCCGG	TGGCTGCCTT	CCCTCCACAG	AAGCAGCAGC	780
AGCAGCAGCA	ACCACAGCAG	CAGCAGCAGC	AGCAGCAGGC	AGCCCTACCC	CAGATGCCGC	840
TCTTTGAGAA	CTTCTATTCC	ATGCCACAGC	AACCTCGCA	GCAACCCCAG	GACTTTGGCC	900
TGCAGCCAGC	TGGGCCACTG	GGACAGTCCC	ACCTGGCTCA	CCACAGCATG	GCACCCCTACC	960
CCTTCCCCCC	CAACCCAGAT	ATGAACCCAG	AACTGCGCAA	GGCCCTTCTG	CAGGACTCAG	1020
CCCCGCAGCC	AGCGCTACCT	CAGGTCCAGA	TCCCCCTCCC	CCGCCGCTCC	CGCCGCCCTCT	1080
CTAAGGAGGG	TATCCTGCCT	CCCAGCGCCC	TGGATGGGGC	TGGCACCCAG	CCTGGGCAGG	1140
AGGCCACTGG	CAACCTGTTC	CTACATCACT	GGCCCCTGCA	GCAGCCGCCA	CCTGGCTCCC	1200
TGGGGCAGCC	CCATCCTGAA	GCTCTGGAT	TCCCCTGGA	GCTGAGGGAG	TCGCAGCTAC	1260
TGCCTGATGG	GGAGAGACTA	GCACCCAATG	GCCGGGAGCG	AGAGGCTCCT	GCCATGGGCA	1320
GCGAGGAGGG	CATGAGGGCA	GTGAGCACAG	GGGACTGTGG	GCAGGTGCTA	CGGGGCGGAG	1380
TGATCCAGAG	CACGCGACGG	AGGCGCCGGG	CATCCCAGGA	GGCCAATTG	CTGACCCCTGG	1440
CCCAGAAGGC	TGTGGAGCTG	GCCTCACTGC	AGAATGCAA	GGATGGCAGT	GGTCTGAAG	1500
AGAAGCGGAA	AAAGTGTATTG	GCCTCAACTA	CCAAGTGTGG	GGTGGAGTTT	TCTGAGCCTT	1560
CCTTAGCCAC	CAAGCGAGCA	CGAGAAAGACA	GTGGGATGGT	ACCCCTCATC	ATCCCAGTGT	1620
CTGTGCTGTG	CGGAACATGTG	GACCCAACCTG	AGGCAGCCCA	GGCTGGAGGT	CTTGATGAGG	1680
ACGGGAAGGG	TCTTGAACAG	AACCTGCTG	AGCACAAGCC	ATCAGTCATC	GTCACCCGCA	1740
GCGGGTCCAC	CCGAATCCCC	GGGACAGATG	CTCAAGCTCA	GCGGGAGGAC	ATGAATGTCA	1800
AGTTGGAGGG	GGAGCCTTCC	GTGCGGAAAC	CAAAGCAGCG	GCCCCAGGCC	GAGCCCCCTCA	1860
TCATCCCCAC	CAAGGCGGGC	ACTTTCATCG	CCCCCTCCGT	CTACTCCAAC	ATCACCCCAT	1920
ACCAGAGCCA	CCTGCGCTCT	CCCGTGCGCC	TAGCTGACCA	CCCCTCTGAG	CGGAGCTTTG	1980
AGCTACCTCC	CTACACGCCG	CCCCCCATCC	TCAGCCCTGT	GCGGGAAGGC	TCTGGCCTCT	2040
ACTTCAATGC	CATCATATCA	ACCAGCACCA	TCCCTGCC	TCCTCCCATC	ACGCCTAAGA	2100
GTGCCCATCG	CACGCTGCTC	CGGACTAAC	GTGCTGAAGT	AACCCCGCCT	GTCCTCTCTG	2160
TGATGGGGGA	GGCCACCCCCA	GTGAGCATCG	AGCCACGGAT	CAACGTGGC	TCCCGGTTCC	2220
AGGCAGAAAT	CCCCTTGATG	AGGGACCGTG	CCCTGGCAGC	TGCAGATCCC	CACAAGGCTG	2280
ACTTGGTGTG	GCAGCCATGG	GAGGACCTAG	AGAGCAGCCG	GGAGAAGCAG	AGGCAAGTGG	2340
AAGACCTGCT	GACAGCCGCC	TGCTCCAGCA	TTTTCCTGG	TGCTGGCACC	AACCAGGAGC	2400
TGGCCCTGCA	CTGCTGAC	GAATCCAGAG	GAGACATCCT	GGAAACGCTG	AATAAGCTGC	2460
TGCTGAAGAA	GCCCCCTGCGG	CCCCACAAACC	ATCCGCTGCC	AACTTATCAC	TACACAGGCT	2520
CTGACCAGTG	GAAGATGGCC	GAGAGGAAGC	TGTTCAACAA	AGGCATTGCC	ATCTACAAGA	2580
AGGATTTCTT	CCTGGTGCAG	AAGCTGATCC	AGACCAAGAC	CGTGGCCCG	TGCGTGGAGT	2640
TCTACTACAC	CTACAAGAAG	CAGGTGAAAA	TCGGCCGCAA	TGGGACTCTA	ACCTTTGGGG	2700
ATGTGGATAC	GAGCGATGAG	AAGTCGGCCC	AGGAAGAGGT	TGAAGTGGAT	ATTAAGACTT	2760
CCCAAAAGTT	CCCAAGGGTG	CCTCTCCCA	GAAGAGAGTC	CCCAAGTGAA	GAGAGGCTGG	2820
AGCCAAGAG	GGAGGTGAAG	GAGCCCAGGA	AGGAGGGGGA	GGAGGAGGTG	CCAGAGATCC	2880
AAGAGAAGGA	GGAGCAGGAA	GAGGGGCGAG	AGCGCAGCAG	GCGGGCAGCG	GCAGTCAAAG	2940
CCACGCAGAC	ACTACAGGCC	AATGAGTCGG	CCAGTGACAT	CCTCATCCTC	CGGAGGCCACG	3000
- AGTCCAACGC	CCCTGGGTCT	GCCGGTGGCC	AGGCCTCGGA	GAAGCCAAGG	GAAGGGACAG	3060
GGAAGTCACG	AAGGGCACTA	CCTTTTCAG	AAAAAAA	AAAAAAACAA	AAAGCTT	3117

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAATTGGCA	CGAGGTCAGT	TTCCTGTGGA	ACACAGAGGC	TGCCTGTCCC	ATTCAAGACAA	60
CGACGGATAC	AGACCAAGGCT	TGCTCTATAA	GGGATCCCAA	CAGTGGATT	GTGTTTAATC	120
TTAATCCGCT	AAACAGTCG	CAAGGATATA	ACGCTCTGTG	CATTGGGAAG	ATTTTATGT	180
TTAATGTCTG	CGGCACAATG	CCTGTCTGTG	GGACCACATCT	GGGAAACCT	GCTCTGGCT	240
GTGAGGCAGA	AAACCAAAC	GAAGAGCTCA	AGAATTGGAA	GCCAGCAAGG	CCAGTCGGAA	300
TTGAGAAAAG	CCTCCAGCTG	TCCACAGAGG	GCTTCATCAC	TCTGACCTAC	AAAGGGCCTC	360
TCTCTGCCAA	AGGTACCGCT	GATGCTTTA	TCGTCGCTT	TGTTTGAAT	GATGATGTT	420
ACTCAGGGCC	CCTCAAATTG	CTGCATCAAG	ATATCGACTC	TGGGCAAGGG	ATCCGAAACA	480
CTTACTTTGA	GTGGAAACC	GCGTTGGCCT	GTGTTCCCTC	TCCAGTGGAC	TGCCAAGTCA	540
CCGACCTGGC	TGGAAATGAG	TACGACCTGA	CTGGCCTAAG	CACAGTCAGG	AAACCTTGGG	600
CGGCTGTTG	CACCTCTGTC	GATGGGAGAA	AGAGGACTTT	CTATTGAGC	GTTGCAATC	660
CTCTCCCTTA	CATTCCGTGA	TGCCAGGGCA	GCGCAGTGGG	GTCTTGCTTA	GTGTCAGAAG	720
GCAATAGCTG	GAATCTGGGT	GTGGTGCAGA	TGAGTCCCCA	AGCCGCGGCG	AATGGATCTT	780
TGAGCATCAT	GTATGTCAAC	GGTGACAAGT	GTGGGAACCA	GCGCTCTCC	ACCAGGATCA	840
CGTTTGAGTG	TGCTCAGATA	TCGGGCTCAC	CAGCATTCA	GCTTCAGGAT	GTTGTCAGT	900
ACGTGTTAT	CTGGAGAACT	GTGGAAGCCT	GTCCCCTGTG	CAGAGTGGAA	GGGGACAAC	960
GTGAGGTGAA	AGACCCAAGG	CATGGCAACT	TGTATGACCT	GAAGCCCCG	GGCCTCAACG	1020
ACACCATCGT	GAGCGCTGGC	GAATACACTT	ATTACTTCCG	GGTCTGTTGG	AAGCTTCCT	1080
CAGACGTCTG	CCCCACAAGT	GACAAGTCCA	AGGTGGTCTC	CTCATGTCA	GAAAAGCGGG	1140
AACCGCAGGG	ATTTCACAAA	GTGGCAGGTC	TCCTGACTCA	GAAGCTAACT	TATGAAAATG	1200
GCTTGTAA	AATGAACCTC	ACGGGGGGGG	ACACTTGCCA	TAAGGTTAT	CAGCGCTCCA	1260
CAGCCATCTT	CTTCTACTGT	GACCGCGGCA	CCCAGCGGCC	AGTATTCTA	AAGGAGACTT	1320
CAGATTGTTG	CTACTTGTG	GAGTGGCGAA	CGCAGTATGC	CTGCCACCT	TTCGATCTGA	1380
CTGAATGTTG	ATTCAAAGAT	GGGGCTGGCA	ACTCCTTCGA	CCTCTCGTCC	CTGTCAAGGT	1440
ACAGTGACAA	CTGGGAAGCC	ATCACTGGG	CGGGGGACCC	GGAGCACTAC	CTCATCAATG	1500
TCTGCAAGTC	TCTGGCCCCG	CAGGCTGGCA	CTGAGCCGTG	CCCTCCAGAA	GCAGCCGCGT	1560
GTCTGCTGGG	TGGCTCCAAG	CCCGTGAACC	TCGGCAGGGT	AAGGGACGGA	CCTCAGTGGG	1620
GAGATGGCAT	AATTGTCCTG	AAATACGTTG	ATGGCGACTT	ATGTCCAGAT	GGGATTCCGG	1680
AAAAGTCAAC	CACCATCCGA	TTCACCTGCA	GCGAGAGCCA	AGTGAACCTC	AGGCCCATGT	1740
TCATCAGCGC	CGTGGAGGAC	TGTGAGTACA	CCTTTGCCTG	GCCCCACAGCC	ACAGCCTGTC	1800
CCATGAAGAG	CAACGAGCAT	GATGACTGCC	AGGTACCAAA	CCCAAGCACA	GGACACCTGT	1860
TTGATCTGAG	CTCCTTAAGT	GGCAGGGCGG	GATTACAGC	TGCTTACAGC	GAGAAGGGGT	1920
TGGTTTACAT	GAGCATCTGT	GGGGAGAATG	AAAACGCCC	TCCTGGCGTG	GGGGCCTGCT	1980
TTGGACAGAC	CAGGATTAGC	GTGGGCAAGG	CCAACAAGAG	GCTGAGATAC	GTGGACCAGG	2040
TCCTGCAGCT	GGTGTACAAG	GATGGGTCCC	CTTGTCCCTC	CAAATCCGGC	CTGAGCTATA	2100
AGAGTGTGAT	CAGTTTCGTG	TGCAGGCCCTG	AGGCCGGGCC	AACCAATAGG	CCCATGCTCA	2160
TCTCCCTGGA	CAAGCAGACA	TGCACTCTCT	TCTTCTCCTG	GCACACGCCG	CTGGCCTGCG	2220
AGCAAGCGAC	CGAATGTTCC	GTGAGGAATG	GAAGCTCTAT	TGTTGACTTG	TCTCCCTTA	2280
TTCATCGCAC	TGGTGGTTAT	GAGGCTTATG	ATGAGAGTGA	GGATGATGCC	TCCGATACCA	2340
ACCCCTGATT	CTACATCAAT	ATTGTCAGC	CACTAAATCC	CATGCACCGA	GTGCCCTGTC	2400
CTGCCGGAGC	CGCTGTGTGC	AAAGTCCCTA	TTGATGGTCC	CCCCATAGAT	ATCGGCCGGG	2460
TAGCAGGACC	ACCAATACTC	AATCCAATAG	CAAATGAGAT	TTACTTGAAT	TTGAAAGCA	2520
- GTACTCCTTG	CCAGGAATTG	AGTTGTAAT	AAAATTGAAC	CTGCTCAACA	GCTGAGGGAG	2580
ACTAGAAATG	ATGGGTCCAT	ATCCTGGTGC	ATTGTCATAC	AATTCAAACA	ATGGTGCAGC	2640
TACCACTTG	TAATTTTAG	GGACTGCAA	CAAGGCTTT	TCTTGAAGCT	GAACCAGAAA	2700
CAACTCTTA	TGTTCTTAG	GCTTTGTAAT	ATGTGCAGGA	ATATATGGAT	ACTGAGGAGG	2760
TTCAAAATTG	GGTCTCCACC	AGTTACCAAT	GCAATCGTCA	ATGACCCAGT	CTTGCAAAAC	2820
TCCCATCCTGA	CGACCCAGTA	TCTCTGTCA	TAAGCGTTT	AGTCCTCAA	CTTCATCTTC	2880
TCCTGGGTTA	AGTTACCCAC	CAGGTAGTTT	GAAGAAAGTT	GTTCCCAGCT	GCACGAGTAA	2940
CACATGGGGT	AGCCGGTGCT	CATGTACAAT	CAGAACCCCT	TCTACAGTCC	TCCTCATTCC	3000
AATTCTTATCA	AATTCTTCCC	TCATGCCTG	AAATCTGGCT	GCAACAGAGC	TGTCCTTCTC	3060
GTAGAGGGGC	TCTTTGTAC	CAAAGTATA	ATTGGTAAGA	GGGTACAGGT	TGATGGTGC	3120
CTCCAGGGGTG	AGGGGCTTCG	TCTGCTGGAT	GTACTTGTG	CCGAACGTAG	TGACCCCCCG	3180
GGGCCAGGCC	GTCTCGCAGC	GATTGGCGGG	TACACAGAC	ATGCTGGCGA	GCTCCGGCGC	3240
TGACGGCGAG	CAGAAAGTGG	CAGGCAGGGT	AGACTTCCC	CGTGCAGGAA	GCCTCGTGCC	3300
GAATTG						3306

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAATTGGCA	CGAGAATGGA	TCAACCTCAA	CAACACGTTA	AAGCTAGACG	AAAGAAGTAA	60
TACACAGTGT	ATGAGTCTCA	CATGAAATAC	CCGGATGTAA	ATCCAAAGAA	ACAGGAAGCA	120
GATTGGTGGT	TGCCAGGGAC	AAGGGCGGTG	GGAGGGAGAAA	ATGGAGAGTA	ACGGGACTTT	180
ACTTTTGGAG	TGATGAGAAT	GTGTTGGAGC	TAGATAGAAG	TGGTGGTGT	ACACCATTGT	240
GGATGTACTA	CCACTTAATT	GTTCACTTAA	AAAGTTAATT	TATGTGAATT	GCATCTTAAT	300
AAAAAACAAAG	GATAACATTC	CAACTCCTGG	ACATTATCCT	TCCTTCCAT	TTGATGTCAG	360
GCCCCGTGTTA	GAATTCTCAT	CCGGTTTGGT	CACTGCACCT	AAGATGTGGA	GAATTAGGA	420
CGCACAGTTA	AGAGGAAGGA	TAACACTGAT	TAAGGTAGTG	CTTTTCTAGG	TTTCCCCTAA	480
ACAAATTAAAC	AGATGGATAG	TGGCACCCT	TACGAGATGG	AAAAACCCAGC	GGAGGAAGA	540
TTTGGGGGAG	AAGTAAAGTT	TGTCTGGGC	CTGTGTTTG	CAACCTGAGT	GTAAAAGACA	600
TATGTAAAGT	CTTCAGTGGC	GAAACACTAA	AACTAGAAAT	GGATCAGAAT	TTTATCTTG	660
GATGTGACTT	CTCAAGGATG	GTCTTGTAC	TTCAGTGCCT	GGTCAAATGA	CAAGATGGC	720
AATCTTTCC	TGAAGGTCCA	AGCACCTGAA	CGTGGCAGGG	TGACCCGATT	CCGATTGCT	780
TAGAACAAATC	CTAGTTCATG	CCTATTGTCC	CTCATGTAAT	TAATATCACT	CTCAAAATGT	840
CTCATTGTTG	GCAATAAAATT	CTGCAACGTG	ATGGCGCAG	TCTCGCGGCC	CGAGCGGCCG	900
GACCTTGTCT	TCGAGGAAGA	GGACCTCCCC	TATGAGGAGG	AAATCATGCG	GAACCAATT	960
TCTGTCAAAT	GCTGGCTTCA	CTACATCGAG	TTCAACACAGG	GCGCCCGAA	GCCCAGGCTC	1020
AATCAGCTAT	ACGAGCGGGC	ACTCAAGCTG	CTGCCCTGCA	GCTACAAACT	CTGGTACCGA	1080
TACCTGAAGG	CGCGTCGGGC	ACAGGTGAAG	CATCGCTGTG	TGACCGACCC	TGCTATGAA	1140
GATGTCAACA	ACTGTATGA	GAGGGCCTTT	GTGTTCATGC	ACAAGATGCC	TCGCTGTGG	1200
CTAGATTACT	GCCAGTTCC	CATGGACCAG	GGGCGCGTCA	CACACACCG	CCGCACCTTC	1260
GACCCTGCC	TCCGGGCACT	GCCCATCACG	CAGCACTCTC	GAATTGGCC	CCTGTATCTG	1320
CGCTTCCCTGC	GCTCACACCC	ACTGCCTGAG	ACAGCTGTGC	GAGGCTATCG	GCGCTTCCTC	1380
AAGCTGAGTC	CTGAGAGTGC	AGAGGAGTAC	ATTGAGTACC	TCAAGTCAG	TGACCGGCTG	1440
GATGAGGCCG	CCCAGCGCCT	GGCCACCGTG	GTGAACGACG	AGCGTTTCGT	GTCTAAGGCC	1500
GGCAAGTCCA	ACTACCAGCT	GTGGCACGAG	CTGTGCGACC	TCATCTCCA	GAATCCGGAC	1560
AAGGTACAGT	CCCTCAATGT	GGACGCCATC	ATCCGCGGGG	GCCTCACCCG	CTTCACCGAC	1620
CAGCTGGCA	AGCTCTGGTG	TTCTCTGCC	GAECTACTACA	TCCGCAGCGG	CCATTTCGAG	1680
AAGGCTCGGG	ACGTGTACGA	GGAGGCCATC	CGGACAGTGA	TGACCGTGC	GGACTTCACA	1740
CAGGTGTTG	ACAGCTACGC	CCAGTTCGAG	GAGAGCATGA	TCGCTGAA	GATGGAGACC	1800
GCCTCGGAGC	TGGGGCGCGA	GGAGGAGGAT	GATGTGGACC	TGGAGCTGC	CCTGGCCCGC	1860
TTCGAGCAGC	TCATCAGCCG	GGGGCCCTG	CTCCTCAACA	GCGTCTTGCT	GCGCCAAAAC	1920
CCACACCACG	TGCACGAGTG	GCACAAGCGT	GTGCCCTGC	ACCAGGGCCG	CCCCCGGGAG	1980
ATCATCAACA	CCTACACAGA	GGCTGTGCA	ACGGTGGACC	CCTTCAGGC	CACAGGCAAG	2040
CCCCACACTC	TGTGGGTGGC	TTTGCCAAG	TTTTATGAGG	ACAACGGACA	GCTGGACGAT	2100
GCCCCTGTCA	TCCTGGAGAA	GGCCACCAAG	GTGAACTTCA	AGCAGGTGGA	TGACCTGGCA	2160
AGCGTGTGGT	GTCAGTGC	AGAGCTGGAG	CTCCGACACG	AGAACTACGA	TGAGGCCTTG	2220
CGGCTGCTGC	GAAAGGCCAC	GGCGCTGCCT	GCCCCGCCGG	CCGAGTACTT	TGATGGTTCA	2280
GAGCCCGTGC	AGAACCGCGT	GTACAAGTCA	CTGAAGGTCT	GGTCCATGCT	CGCCGACCTG	2340
GAGGAGAGCC	TCGGCACCTT	CCAGTCCACC	AAGGCCGTG	ACGACCGCAT	CCTGGACCTG	2400
CGTATCGCAA	CACCCAGAT	CGTCATCAAC	TATGCCATGT	TCCTGGAGGA	GCACAAGTAC	2460
TTCGAGGAGA	GCTTCAAGGC	GTACGAGCGC	GGCATCTCGC	TGTTCAAGTG	GCCCAACGTG	2520
TCCGACATCT	GGAGCACCTA	CCTGACCAA	TTCATTGCC	GCTATGGGG	CCGCAAGCTG	2580
GAGCGGGCAC	GGGACCTGTT	TGAACAGGCT	CTGGACGGCT	GCCCCCCTAA	ATATGCCAAG	2640
ACCTTGTACC	TGCTGTACGC	ACAGCTGGAG	GAGGAGTGGG	GCCTGGCCCG	GCATGCCATG	2700
GCCGTGTACG	AGCGTGCCAC	CAGGGCCGTG	GAGCCCCCCC	AGCAGTATGA	CATGTTCAAC	2760

ATCTACATCA	AGCGGGCGGC	CGAGATCTAT	GGGGTCACCC	ACACCCGCGG	CATCTACCAG	2820
AAGGCCATTG	AGGTGCTGTC	GGACGAGCAC	GCGCGTGAGA	TGTGCCTGCG	GTTGCAGAC	2880
ATGGAGTGCA	AGCTCGGGGA	GATTGACCGC	GCCCCGGGCCA	TCTACAGCTT	CTGCTCCCAG	2940
ATCTGTGACC	CCCGGACGAC	CGGCGCGTTC	TGGCAGACGT	GGAAGGACTT	TGAGGTCCGG	3000
CATGGCAATG	AGGACACCAT	CAAGGAAATG	CTGCGTATCC	GGCGCAGCGT	GCAGGCCACG	3060
TACAACACGC	AGGTCAACTT	CATGGCCTCG	CAGATGCTCA	AGGTCTCGGG	CAGTGCCACG	3120
GGCACCGTGT	CTGACCTGGC	CCCTGGGCAG	AGTGGCATGG	ACGACATGAA	GCTGCTGGAA	3180
CAGCGGGCAG	AGCAGCTGGC	GGCTGAGGCG	GAGCGTGACC	AGCCCTTGCG	CGCCCAGAGC	3240
AAGATCCTGT	TCGTGAGGAG	TGACGCCCTCC	CGGGAGGAGC	TGGCAGAGCT	GGCACAGCAG	3300
GTCAACCCCG	AGGAGATCCA	GCTGGGCGAG	GACGAGGACG	AGGACGAGAT	GGACCTGGAG	3360
CCCAACGAGG	TTCGGCTGGA	GCAGCAGAGC	GTGCCAGCCG	CAGTGTGTTGG	GAGCCTGAAG	3420
GAAGACTGAC	CCGTCCCCTC	GTGCCGAATT	CGGCACGAGC	AAGACCAGCC	CCCAGATCAT	3480
TTGCCTCAAA	GGTTTCCCT	CGAAGTCACA	AATGTTCAA	GAATCTCAA	ATTTTACAAA	3540
GTTTGAAGTG	TGGGCATTGG	TGGCCTGTGG	CTGTGTCCTC	TCTCTGTAGC	TGTTTTCTCC	3600
CTACATCCCT	GAAAGGAAGT	TGAGCCTGCT	CCTCCATCCG	CAGACCTCCC	TTTCCAGCGC	3660
CCAGGGCAGT	GGGTGCTGTG	AGGGCAGCAT	GCTAGGTGTG	ACCGTGCCTC	TGGCCTCCAG	3720
GCCCCGTGTCC	CTCTGTCCTC	TAGCCCACTA	AGGCCCTGGC	CCATTTGTGC	TAACACAGGCA	3780
GTCGGACCTA	GAAAGAGCAG	ACAATCTCTC	TGGGTCACCA	GTCTGGCTAG	GAGCTGGTCT	3840
CCTGACTGGG	ATCCAGGCCT	TCTCCCCTGC	CCATGTGAAT	TCCCAGGGC	AGAGCCTGAA	3900
ATGTTGAACA	CAGCACTGGC	CAAAGAGATG	TCACCGTGGG	AACCGAGGCT	CTCTTCTCCT	3960
CCTGCCTGCT	TCAGTGGGTT	CAGAGTAGCT	GAGGCTTGTC	TGAGAGGAGT	TGGAGTGCTG	4020
GTTTTCACCC	TGGTTGGTGT	GCTTGCTTT	GAGGGCACTT	AGAAAGCCCA	GCCCAGCCCT	4080
TGCTCCTGCC	CTGCACACAG	CGGAGCGACT	TTCTAGGTA	TGCTCTTGAT	TTCTGCAGAA	4140
GCAGCAGGTG	GCATGGAGCC	AAGAGGAAGT	GTGACTGAAA	CTGTCCACTC	ATAGCCCGGC	4200
TGCCGTATTG	AGAGGGCT					4218

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAGCTCGCGC	GCCTGCGAGGT	CGACACTAGT	GGATCCAAAG	AATTGGCAC	GAGGGAAACT	60
CAACGGTGT	CGAGTGGGAGG	ACAGGGACAG	AGCCCTCTGT	GGTGGAACGA	CCCCACCTCG	120
AGGAGCTTCC	TGAGCAGGTG	GCAGAAAGATG	CGATTGACTG	GGGCGACTTT	GGGGTAGAGG	180
CAGTGTCTGA	GGGGACTGAC	TCTGGCATCT	CTGCCGAGGC	TGCTGGAATC	GACTGGGGCA	240
TCTTCCCAGGA	ATCAGATTCA	AAGGATCCTG	GAGGTGATGG	GATAGACTGG	GGAGACGATG	300
CTGTTGCTTT	GCAGATCACA	GTGCTGGAAG	CAGGAACCCA	GGCTCCAGAA	GGTGTGCCA	360
GGGGCCCAGA	TGCCCTGACA	CTGCTTGAAT	ACACTGAGAC	CCGGAATCAG	TTCCCTTGATG	420
AGCTCATGGA	GCTTGAGATC	TTCTTAGGCC	AGAGAGCAGT	GGAGTTGAGT	GAGGAGGCAG	480
ATGTCCTGTC	TGTGAGCCAG	TTCCAGCTGG	CTCCAGCCAT	CCTGCAGGGC	CAGACCAAAG	540
AGAAGATGGT	TACCATGGTG	TCAGTGTG	AGGATCTGAT	TGGCAAGCTT	ACCAAGTCTTC	600
AGCTGCAACA	CCTGTTTATG	ATCCTGGCCT	CACCAAGTA	TGTGGACCGA	GTGACTGAAT	660
TCCTCCAGCA	AAAGCTGAAG	CAGTCCCAGC	TGCTGGCTTT	GAAGAAAGAG	CTGATGGTGC	720
AGAAGCAGCA	GGAGGCACCTT	GAGGAGCAGG	CGGCTCTGGA	GCCTAAGCTG	GACCTGCTAC	780
TGGAGAAGAC	CAAGGAGCTG	CAGAAGCTGA	TTGAAGCTGA	CATCTCCAAG	AGGTACAGCG	840
GGCGCCCTGT	GAACCTGATG	GGAACCTCTC	TGTGACACCC	TCCGTGTTCT	TGCCTGCCCA	900
TCTTCTCCGC	TTTTGGGATG	AAGATGATAG	CCAGGGCTGT	TGTTTTGGGG	CCCTTCAAGG	960
CAAAAGACCA	GGCTGACTGG	AAGATGGAAA	GCCACAGGAA	GGAAGCAGGCA	CCTGATGGTG	1020
ATCTTGGCAC	TCTCCATGTT	CTCTACAAGA	AGCTGTGGTG	ATTGGCCCTG	TGGTCTATCA	1080
GGCGAAAACC	ACAGATTCTC	CTTCTAGTTA	GTATAGCGCA	AAAAGCTTCT	CGAGAGTACT	1140

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCCTCACTAA	AGGGAACAAA	AGCTGGAGCT	CGCGCGCCTG	CAGGTCGACA	CTAGTGGATC	60
GAAAGTTCGT	TACGCCAAGC	TCGAAATTAA	CTCTGGGCTG	ACCCATAAAC	ATTGTCTGA	120
TCTAGGATAT	AGTTGCGTTT	CTTGCAGGCA	GCAATCTGGA	TGAGGCGGTT	GAGGCAGTGG	180
GTGGCCTGCT	GGATCAGGAC	ATCCCAGCGG	CCAGCATAGT	TCCGCTGCCG	GCGTAGGCC	240
ATCACCCGCA	TCTTATCCAT	GATGGCATTG	GTACCCAGGA	TGTTGTACTT	CTTGGAAAGGG	300
TTGGAGGCTG	CATGTTGAT	GGCCCATGTG	GTCTTGCCAG	CAGCAGGCAG	GCCCACCATC	360
ATCAGAAATCT	CACATTCTGC	CTTGCTCTT	GGTCCAACGG	TGCCCCGGAT	ACGCTCACTA	420
AGGGGAAGGT	GCTGGATGAA	GGTAAACCCC	GGGAGGACAG	AACAGTAGGG	CTCTGCTCTC	480
TGTCCGAAGT	TGAACCTCAC	TGCGCAATTG	TTCACCAGGA	CATGAGGATA	GAGGGCCTGA	540
CCCCCAAGG	CTTCCTTCTG	GATTGGAAA	GCAATGCCA	TCCACTTTC	ATTCTGGTA	600
AAAGACAGTT	CCACGTCATT	TCCACATTCA	AAATCCGAA	AGCAGCCAAT	CACCGGAGAG	660
CTCTGCGGTG	CTAGGAGAGC	GGCTGGGCC	GCAGACTGGG	GGGAAAGCTC	CGCAGCCGCA	720
GTGGGCCCCA	GGATCAGGCC	CCGCCTGGCC	TGGAGAAGCC	CAGTCTGGC	TGGAGCAGGA	780
GCTGGACAGT	GTGGCCTTGC	GTTCGCCCC	GGGAGCGCTG	CGAGTGTGCG	GGCCTCGGGT	840
GGATTTGCTG	AGCACCAATA	CCTCACGGTT	GCCAACCTGG	GGTTTTAGCT	CCCTTGGTTT	900
TAATCCCCTA	GGGGCGGGTG	GGGGCACCGG	AGGAAGGATG	GGCCAGCTGG	GTGCAATCCT	960
GCTGTAAGCC	AGCCATTCTC	TGATTCTTA	GAATTAAC	AACGGTGC	CCGGAGGCCG	1020
CGGGGGCCGG	AGCGGAGCAG	CCGCGGCTGA	GGTCCCGAG	TCGGCCGCTC	GGGGCTGCGC	1080
TCCGCCGCGG	GGACCCCCGGC	CTCTGGCCGC	GCCGGCTCCG	GCCTCCGGGG	GGGCCGGGGC	1140
CGCCGGGACA	TGGTGCCAGT	CGCACCCCTT	CCCCGCCGCC	GCTGAGCTCG	CCGGCCGCGC	1200
CCGGGCTGGG	ACGTCCGAGC	GGGAAGATGT	TTTCCGCC	GAAGAAGCTG	GTGGGGTCGG	1260
ACCAGGCC	GGGCCGGGAC	AAGAACATCC	CCGCCGGGCT	GCAGTCCATG	AACCAGGCC	1320
TGCAGAGGCG	CTTCGCCAAG	GGGGTGCAGT	ACAACATGAA	GATAGTGATC	CGGGGAGACA	1380
GGAACACGGG	CAAGACAGCG	CTGTGGCACC	GCCTGCAGGG	CCGGCCGTT	GTGGAGGAGT	1440
ACATCCCCAC	ACAGGAGATC	CAGGTACCA	GCATCCACTG	GAGCTAACAG	ACCACGGATG	1500
ACATCGTGA	GGTTGAAGTC	TGGGATGTAG	TAGACAAAGG	AAAATGCAA	AAGCGAGGCG	1560
ACGGCTTAA	GATGGAGAAC	GACCCCCAGG	AGNCGGAGTC	TGAAATGGCC	CTGGATGCTG	1620
AGTTCCCTGGA	CGTGTACAAG	AACTGCAACG	GGGTGGTCAT	GATGTTCGAC	ATTACCAAGC	1680
- AGTGGACCTT	CAATTACATT	CTCCGGGAGC	TTCCAAAAGT	GCCCACCCAC	GTGCCAGTGT	1740
CGCTGCTGGG	GAACATACCGG	GACATGGGCG	AGCACCGAGT	CATCCTGCCG	GACGACGTGC	1800
GTGACTTCAT	CGACAAACCTG	GACAGACCTC	CAGGTTCCCTC	CTACTTCCGC	TATGCTGAGT	1860
CTTCCATGAA	GAACAGCTTC	GGCCTAAAGT	ACCTTCATAA	GTTCTCAAT	ATCCCATT	1920
TGCAGCTTC	GAGGGAGACG	CTGTTGCAGG	AGCTGGAGAC	GAACCAGCTG	GACATGGACG	1980
CCACGCTGG	GGAGCTGTG	GTGCAGCAGG	AGACGGAGGA	CCAGAACTAC	GGCATCTTCC	2040
TGGAGATGAT	GGAGGCTCGC	AGCCGTGGCC	ATGCGTCCC	ACTGGCGGCC	AACGGGCAGA	2100
GCCCCATCCCC	GGGCTCCAG	TCACCAGTCC	TGCCTGCACC	CGCTGTGTC	ACGGGGAGCT	2160
CCAGCCCCGG	CACACCCAG	CCCGCCCCAC	AGCTGCCCT	CAATGCTGCC	CCACCATCCT	2220
CTGTGCC	TGTACCACCC	TCAGAGGCC	TGCCCCCACC	TGCGTCCCC	TCAGCCCCCG	2280
CCCCACGGCG	CAGCATCATC	TCTAGGCTGT	TTGGGACGTC	ACCTGCCACC	GAGGCAGCCC	2340
CTCCACCTCC	AGAGCCAGTC	CCGGCCGAC	AGGGCCAGC	AACGGTCCAG	AGTGTGGAGG	2400
ACTTTGTTCC	TGACGACCGC	CTGGACCGCA	GCTTCCTGGA	AGACACAACC	CCCGCCAGGG	2460
ACGAGAAGAA	GGTGGGGGCC	AAGGCTGCC	AGCAGGACAG	TGACAGTGT	GGGGAGGCC	2520
TGGCGGCAA	CCCGATGGTG	GCAGGGTTCC	AGGACGATGT	GGACCTCGAA	GACCAGCCAC	2580

SEQUENCE ID: 10

GTGGGAGTCC	CCCGCTGCCT	GCAGGCCCG	TCCCCAGTCA	AGACATCACT	CTTCGAGTG	2640
AGGAGGAAGC	AGAAGTGGCA	GCTCCCACAA	AAGGCCCTGC	CCCAGCTCCC	CAGCAGTGCT	2700
CAGAGCCAGA	GACCAAGTGG	TCCTCCATAC	CAGCTTCGAA	GCCACGGAGG	GGGACAGCTC	2760
CCACGAGGAC	CGCAGCACCC	CCCTGGCCAG	GCGGTGTCTC	TGTTCGCACA	GGTCCGGAGA	2820
AGCGCAGCAG	CACCAAGGCC	CCTGCTGAGA	TGGAGCCGGG	GAAGGGTGAG	CAGGCCTCCT	2880
CGTCGGAGAG	TGACCCCCGAG	GGACCCATTG	CTGCACAAAT	GCTGTCCTTC	GTCATGGATG	2940
ACCCCGACTT	TGAGAGCGAG	GGATCAGACAA	CACAGCGCAG	GGCGGATGAC	TTTCCCCTGC	3000
GAGATGACCC	CTCCGATGTG	ACTGACGAGG	ATGAGGGCCC	TGCCGAGCCG	CCCCCACCCC	3060
CCAAGCTCCC	TCTCCCCGCC	TTCAGACTGA	AGAATGACTC	GGACCTCTTC	GGGCTGGGGC	3120
TGGAGGAGGC	CGGACCCAAG	GAGAGCAGTG	AGGAAGGTAA	GGAGGGCAAA	ACCCCTCTA	3180
AGGAGAAGAA	AAAAAAAACA	AAAAGCTTCT	CGAGAGTACT	TCTAGAGCGG	CCGCGGGCCC	3240
ATCGATTTTC	CACCCGGGTG	GGGTACCAAGG	TAAGTGTACC	CAATTGCCCC	TATAAGTGAGT	3300
CGTATT						3306

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGCGGGGCCA GAGTGGGCTG 20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCAGTCCTGG CCTGCGGATG 20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTCGACAGGA GAATTGGTTC 20

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCCTGGGTTC GGTGCGGGAC

20

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TGGTCGGGTG TTTGTGAGTG

20

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCTCTTCCGT CTCCTCAGTG

20

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGATTGCTAG TCTCACAGAC

20

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTAAGGGTGG CTGAAGGGAC

20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ACCTTCCCTC CCTGTCACAG

20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGGTCGGGTG TTTGTGAGTG

20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ACACCATTCC AGAAATTAG

20

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAACTGCAGG TGGCTGAGTC

20

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTCCTAATGT TTTCAGGGAG

20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AAAACCTATG GTTACAATTG

20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TCCTAGACAT GGTTCAAGTG

20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GATATAATTA GTTCTCCATC

20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGCCTGTTC CAGGCTGCAC

20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGACGGCGAC CTCCACCCAC

20

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGGCTCCTCC GACGCCTGAG

20

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

- AGTCTAGCCC TGGCCTTGAC

20

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

GTC ACTGGGG ACTCCGGCAG

20

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CAGCTTCCCC TGGGCACATG

20

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CACAGCTGTC TCAAGCCCCAG

20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ACTGTTCCCC CTACATGATG

20

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATCATATCCT CTTGCTGGTC

20

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GTTCAGAG CTTGTCTGTG

20

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTTCAGAG CTCATAGTTG

20

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TAGCAGGGAG CCATGACCTG

20

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CTTGGCGCCA GAAGCGAGAG

20

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCTCTCTCTC TCTCTCTCTC

20

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TCCCCGCTGA TTCCGCCAAG

20

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTTTTGAAAT TCGGCACGAG

20

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CCCCTGGTCC GCACCAGTTC

20

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAGAAGGGTC GGGGCAG

20

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AAATCACATC GCGTCAACAC

20

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TAAGAGAGTC ATAGTTACTC

20

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GCTCTAGAAG TACTCTCGAG

20

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ACTCTGGCCA TCAGGAGATC

20

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CAGGCGTTGT AGATGTTCTG

20

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AGTGGCAGGC AGAAGTAATG

20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGTTGGAGAA CTGGATGTAG

20

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CTATTCAGAT GCAACGCCAG

20

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CCATGGCACA CAGAGCAGAC

20

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GCTACCATGC AGAGACACAG

20

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CAGGCTGACA AGAAAATCAG

20

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCACGCATA GAGGAGAGAC

20

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TGGGTGATGC CTTTGCTGAC

20

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AAAACAAGAT CAAGGTGATG

20

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TGCCCCACAT TGCTATGGTG

20

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GACCAAGATC AGAAGTAGAG

20

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

- CCCCTGGGCC AATGATGTTG

20

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TCTTCCCACC ATAGCAATG

19

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TGGTCTTGGT GACCAATGTG

20

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACACCTCGGT GACCCCTGTG

20

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TCTCCAAGTT CGGCACAGTG

20

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ACATGGGCTG CACTCACGAC

20

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GATCCTCTGA ACCTGCAGAG

20

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GGAAATGAGG TGGGGCGATC

20

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTTGCCCTTG GACAAGGATG

20

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GCACCTGCCA TTGGGGGTAG

20

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GGTGGAAAGCC ATTGACGGTG

20

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TGCGTCTCTC GTCGCTGCTG

20

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GCGGAAACTC TGTGGTGCTG

20

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

AGGATTGCCT TCCTCTACTG

20

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TGTCTGTTTC ACCAGGGCAG

20

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CCAGTGCCTC TATGCATGTC

20

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

AGGAAGCCCCA CGCACACCAAC

20

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CCCTTTGTTC CCTGATCTTC

20

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CGCTCGGGAT CCAGGGTCATC

20

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TCGAGGTTCA GAGCGTAGTG

20

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TCTTGGATCT CTGGCACCTC

20

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CCATCAGAGT GAAGGAGGAG

20

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CCATCTTCCA CTGGTCAGAG

20

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CTCCTTCTCT TGGATCTCTG

20

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TTACTTCAGC ACTGTTAGTC

20

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AGGGAGGTAG CTCAAAGCTC

20

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TGGGTCCACA GTTCGCCACAG

20

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CAACTCTGTG ATGGCTCCAG

20

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

AGCAGGGTTC TGTTCAAGAC

20

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CCATTGGGTG CTAGTCTCTC

20

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

CAGCCATGCT GTCCCAGCAG

20

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

- CTGGACCTGA GGTAGCGCTG

20

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATAACCACCC TGAGGCCACTG

20

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCTGCAGGTC GACACTAGTG

20

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AATTGGAATG AGGAGGACTG

20

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GCTCTAGAAG TACTCTCGAG

20

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ATTGTATGAC AATGCACCAAG

20

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

TCCACAGAGG GCTTCATCAC

20

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

CCTGACTGGC CTAAGCACAG

20

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

AAGCCTCATA ACCACCAGTG

20

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TGTCAACGGT GACAAGTGTG

20

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TTGTACACCA GCTGCAGGTC

20

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GGGTGTGGTG CAGATGAGTC

20

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

ATCACACTCT TATAGCTCAG

20

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GTGGGAAGCT TTCCTCAGAC

20

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TGATGAACAT GGGCCTGGAG

20

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CATTGTGGAT GTACTACCAC

20

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

TGTGTTTGAC AACCTGAGTG

20

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

ATAGTGGCAC CACTTACGAG

20

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

AATTCTGCAA CGTGATGGCG

20

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

CACAAGATGC CTCGTCTGTG

20

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

AATCCGGACA AGGTACAGTC

20

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GCACGAGTGG CACAAGCGTG

20

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GCAAGCGTGT GGTGTCAGTG

20

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

TGTTTGAACA GGCTCTGGAC

20

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CGGCATGGCA ATGAGGACAC 20

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

AGGACGAGAT GGACCTCCAG 20

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CCCTCTGTCC TCTAGCCCAC 20

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TCTTGAGGGG ACTGACTCTG 20

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TGAGTGAGGA GGCAGATGTC

20

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TGGCTTGAA GAAAGAGCTG

20

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GCAAAAGACC AGGCTGACTG

20

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TGCAGCTCCT TGGTCTTCTC

20

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GATTCACAGT CCCAAGGCTC

20

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ATCTGGATGA GGCGGTTGAG

20

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GGTCACTCTC CGACGAGGAG

20

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GGATCCAAAG TTCGTCTCTG

20

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CGCTGTGTGT CTGATCCCTC

20

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ATGAAGGTAA ACCCCGGGAG

20

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

TGGTCTCTGG CTCTGAGCAC

20

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GCCTGGAGAA GCCCAGTCTG

20

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

CACACTCTGG ACCGTTGCTG

20

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

AAAGCTCCGC AGCCGCAGTG

20

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

TCTTCCAGGA AGCTGCGGTC

20

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GATGGTGGGG CAGCATTGAG

20

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GTCACCAGTG GTGCCTGCAG

20

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ACCTCACGGT TGCCAACCTG

20

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:
CGAACACAGCG TCTCCCTCTG 20

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:
AGTACCTTCA TAAAGTTCTTC 20

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:
TCCCAAGACTT CAACCTTCAC 20

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:
AACATCTTC CCGGTCGGAC 20

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GCTGAGCACC TTTACCTCAC

20

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GACGTCCGTC CGGGAAGATG

20

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ACACAGGAGA TGCAGGTCAC

20

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GAGTCTTCCA TGAAGAACAG

20

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GCAGTGAGGA AGGTAAGGAG

20

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4047 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 378...1799
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GGATCCAAAG GACGCCCG CCGACAGGAG AATTGGTTCC CGGGCCCGCG GCGATGCC	60
CCCGGTAGCT CGGGCCCGTG GTCGGGTGTT TGTGAGTGT TCTATGTGGG AGAAGGAGGA	120
GGAGGAGGAA GAAGAACAA CGATTGTCT TCTCGGCTGG TCTCCCCCG GCTCTACATG	180
TTCCCCGAC TGAGGAGACG GAAGAGGAGC CGTAGCCGCC CCCCTCCCG GCCCGGATTA	240
TAGTCTCTCG CCACAGCGGC CTCGGCCTCC CCTTGGATTAGACGCCGAT TCGCCCAGTG	300
TTTGGGAAAT GGGAAAGTAAT GACAGCTGGC ACCTGAACTA AGTACTTTA TAGGCAACAC	360
CATTCCAGAA ATTCAAGG ATG AAT GGG GAT ATG CCC CAT GTC CCC ATT ACT	410
Met Asn Gly Asp Met Pro His Val Pro Ile Thr	
1 5 10	
ACT CTT GCG GGG ATT GCT AGT CTC ACA GAC CTC CTG AAC CAG CTG CCT	458
Thr Leu Ala Gly Ile Ala Ser Leu Thr Asp Leu Leu Asn Gln Leu Pro	
15 20 25	
CTT CCA TCT CCT TTA CCT GCT ACA ACT ACA AAG AGC CTT CTC TTT AAT	506
Leu Pro Ser Pro Leu Pro Ala Thr Thr Thr Lys Ser Leu Leu Phe Asn	
30 35 40	
GCA CGA ATA GCA GAA GAG GTG AAC TGC CTT TTG GCT TGT AGG GAT GAC	554
Ala Arg Ile Ala Glu Glu Val Asn Cys Leu Leu Ala Cys Arg Asp Asp	
45 50 55	
AAT TTG GTT TCA CAG CTT GTC CAT AGC CTC AAC CAG GTA TCA ACA GAT	602
Asn Leu Val Ser Gln Leu Val His Ser Leu Asn Gln Val Ser Thr Asp	
60 65 70 75	
CAC ATA GAG TTG AAA GAT AAC CTT GGC AGT GAT GAC CCA GAA GGT GAC	650
His Ile Glu Leu Lys Asp Asn Leu Gly Ser Asp Asp Pro Glu Gly Asp	
80 85 90	
ATA CCA GTC TTG TTG CAG GCC GTC CTG GCA AGG AGT CCT AAT GTT TTC	698
Ile Pro Val Leu Leu Gln Ala Val Leu Ala Arg Ser Pro Asn Val Phe	
95 100 105	
AGG GAG AAA AGC ATG CAG AAC AGA TAT GTA CAA AGT GGA ATG ATG ATG	746
Arg Glu Lys Ser Met Gln Asn Arg Tyr Val Gln Ser Gly Met Met Met	
110 115 120	
TCT CAG TAT AAA CTT TCT CAG AAT TCC ATG CAC AGT AGT CCT GCA TCT	794
Ser Gln Tyr Lys Leu Ser Gln Asn Ser Met His Ser Ser Pro Ala Ser	
125 130 135	
TCC AAT TAT CAA CAA ACC ACT ATC TCA CAT AGC CCC TCC AGC CGG TTT	842

Ser	Asn	Tyr	Gln	Gln	Thr	Thr	Ile	Ser	His	Ser	Pro	Ser	Ser	Arg	Phe	
140					145				150					155		
GTG	CCA	CCA	CAG	ACA	AGC	TCT	GGG	AAC	AGA	TTT	ATG	CCA	CAG	CAA	AAT	890
Val	Pro	Pro	Gln	Thr	Ser	Ser	Gly	Asn	Arg	Phe	Met	Pro	Gln	Gln	Asn	
					160				165					170		
AGC	CCA	GTG	CCT	AGT	CCA	TAC	GCC	CCA	AGC	CCT	GCA	GGA	TAC	ATG		938
Ser	Pro	Val	Pro	Ser	Pro	Tyr	Ala	Pro	Gln	Ser	Pro	Ala	Gly	Tyr	Met	
					175				180					185		
CCA	TAT	TCC	CAT	CCT	TCA	AGT	TAC	ACA	ACA	CAT	CCA	CAG	ATG	CAA	CAA	986
Pro	Tyr	Ser	His	Pro	Ser	Ser	Tyr	Thr	Thr	His	Pro	Gln	Met	Gln	Gln	
					190				195					200		
GCA	TCG	GTA	TCA	AGT	CCC	ATT	GTT	GCA	GGT	GGT	TTG	AGA	AAC	ATA	CAT	1034
Ala	Ser	Val	Ser	Ser	Pro	Ile	Val	Ala	Gly	Gly	Leu	Arg	Asn	Ile	His	
					205				210					215		
GAT	AAT	AAA	GTT	TCT	GGT	CCG	TTG	TCT	GGC	AAT	TCA	GCT	AAT	CAT	CAT	1082
Asp	Asn	Lys	Val	Ser	Gly	Pro	Leu	Ser	Gly	Asn	Ser	Ala	Asn	His	His	
					220				225					230		235
GCT	GAT	AAT	CCT	AGA	CAT	GGT	TCA	AGT	GAG	GAC	TAC	CTA	CAC	ATG	GTG	1130
Ala	Asp	Asn	Pro	Arg	His	Gly	Ser	Ser	Glu	Asp	Tyr	Leu	His	Met	Val	
					240				245					250		
CAC	AGG	CTA	AGT	AGT	GAC	GAT	GGA	GAT	TCT	TCA	ACA	ATG	AGG	AAT	GCT	1178
His	Arg	Leu	Ser	Ser	Asp	Asp	Gly	Asp	Ser	Ser	Thr	Met	Arg	Asn	Ala	
					255				260					265		
GCA	TCT	TTT	CCC	TTG	AGA	TCT	CCA	CAG	CCA	GTA	TGC	TCC	CCT	GCT	GGA	1226
Ala	Ser	Phe	Pro	Leu	Arg	Ser	Pro	Gln	Pro	Val	Cys	Ser	Pro	Ala	Gly	
					270				275					280		
AGT	GAA	GGA	ACT	CCT	AAA	GGC	TCA	AGA	CCA	CCT	TTA	ATC	CTA	CAA	TCT	1274
Ser	Glu	Gly	Thr	Pro	Lys	Gly	Ser	Arg	Pro	Pro	Leu	Ile	Leu	Gln	Ser	
					285				290					295		
CAG	TCT	CTA	CCT	TGT	TCA	TCA	CCT	CGA	GAT	GTT	CCA	CCA	GAT	ATC	TTG	1322
Gln	Ser	Leu	Pro	Cys	Ser	Ser	Pro	Arg	Asp	Val	Pro	Pro	Asp	Ile	Leu	
					300				305					310		315
CTA	GAT	TCT	CCA	GAA	AGA	AAA	CAA	AAG	AAG	CAG	AAG	AAA	ATG	AAA	TTA	1370
Leu	Asp	Ser	Pro	Glu	Arg	Lys	Gln	Lys	Lys	Gln	Lys	Lys	Lys	Met	Lys	
					320				325					330		
GGC	AAG	GAT	GAA	AAA	GAG	CAG	AGT	GAG	AAA	GCG	GCA	ATG	TAT	GAT	ATA	1418
Gly	Lys	Asp	Glu	Lys	Glu	Gln	Ser	Glu	Lys	Ala	Ala	Met	Tyr	Asp	Ile	
					335				340					345		
ATT	AGT	TCT	CCA	TCC	AAG	GAC	TCT	ACT	AAA	CTT	ACA	TTA	AGA	CTT	TCT	1466
Ile	Ser	Ser	Pro	Ser	Lys	Asp	Ser	Thr	Lys	Leu	Thr	Leu	Arg	Leu	Ser	
					350				355					360		
CGT	GTA	AGG	TCT	TCA	GAC	ATG	GAC	CAG	CAA	GAG	GAT	ATG	ATT	TCT	GGT	1514
Arg	Val	Arg	Ser	Ser	Asp	Met	Asp	Gln	Gln	Glu	Asp	Met	Ile	Ser	Gly	

365

370

375

GTG GAA AAT AGC AAT GTT TCA GAA AAT GAT ATT CCT TTT AAT GTG CAG	1562
Val Glu Asn Ser Asn Val Ser Glu Asn Asp Ile Pro Phe Asn Val Gln	
380 385 390 395	
TAC CCA GGA CAG ACT TCA AAA ACA CCC ATT ACT CCA CAA GAT ATA AAC	1610
Tyr Pro Gly Gln Thr Ser Lys Thr Pro Ile Thr Pro Gln Asp Ile Asn	
400 405 410	
CGC CCA CTA AAT GCT GCT CAA TGT TTG TCG CAG CAA GAA CAA ACA GCA	1658
Arg Pro Leu Asn Ala Ala Gln Cys Leu Ser Gln Gln Glu Gln Thr Ala	
415 420 425	
TTC CTT CCA GCA AAT CAA GTG CCT GTT TTA CAA CAG AAC ACT TCA GTT	1706
Phe Leu Pro Ala Asn Gln Val Pro Val Leu Gln Gln Asn Thr Ser Val	
430 435 440	
GCT GCA AAA CAA CCC CAG ACC AAT AGT CAC AAA ACC TTG GTG CAG CCT	1754
Ala Ala Lys Gln Pro Gln Thr Asn Ser His Lys Thr Leu Val Gln Pro	
445 450 455	
GGA ACA GGC ATA GAG GTC TCA GCA GAG CTG CCC AAG GAC AAG ACC TAAGA	1804
Gly Thr Gly Ile Glu Val Ser Ala Glu Leu Pro Lys Asp Lys Thr	
460 465 470	
TCCAGCAGGG AACTATGTAG TCACCCCGAG AGGCCAGCT CTCTCCGTGA GCTCTGGGCC	1864
TAGGGTGGGG GTGGTTGTTG GTTCTGCGCG CACTGTTCCC CCTACATGAT GGGTCCATCC	1924
CAGTTGGCTT CTCTCACTCG CTTCCCTCTG TGGAGAAGCC TGTCCAGGTG TCACTGCCTC	1984
CAGGAAGCTG TCTCTGATTCTCCAGTTGA ACAGTGAGAT TTGCCACACC TCACATGCAT	2044
CGCTCTTGTCTCCAGTTGA ACAGTGAGAT TTGCCACACC TCACATGCAT	2104
GGCTTCCAC TTGAGTCTCC CTGGTGGAGC CCAGCTCCTG ACATACCTGG TAAAAGTTCT	2164
CAAGAGAAGA ACATGGAGGA GGAATGTGGA TAACAACCTT GGCTGCCTGT GTGTTCCAAG	2224
CTAGGAAGAT GTAATGTCCC CACAAACGGG GTAAATGGCT TGCCCTCGTC ACAGCTGTCT	2284
CAAGCCCAGG CCCTGGGCCG CAGCCCAAGC CCAAGGACTA GGTCCAGAGC CACACAGCCG	2344
CAGGCCACAT CCGCTCACC TGGGACCCCTT TGTGGGGTAC AGTCTCCGGC CCCACCCAGA	2404
CCTCCTGAAG GAGAGACCCC ATGGCAAGGA CTCAGCCACC TGCAGTTCA TAAGCCCCA	2464
GTGGGTTCCCT AGGCATGAAG ACCACCGGTT AGAGGCTGAA CTGGCAGGAA CCTGTCTCCA	2524
GCCCCTCTC ACCCCAGCCG GGCCCTGCCT CAGAGGCAGC ACCCAGGACG TGGCCATGAC	2584
CCGTGGACTC CACTCAATCC CTCTTCTCCA GGAGCCATGC AAAGTGTCAAG CCAGCCAGGC	2644
CCCTGGAAGG CAGTCATCAC CTCTTAAGGC ATTGTGGGTG TCGGTCTGC AACTGCCAGG	2704
TGCAGCACAC GACCCGTGTC CGGTGTTCGA TAGCAGGGAG CCATGACCTG GCAACGATT	2764
CACGCTAAAGGGGACCCCG GGGGGCCCTG GGTGGGGCG GATCAGCTTT CCCTGGGCAC	2824
ATCTGCCTCA TTCCAGATCT CCAGGGCTCA TGTCTGTGAC AGGGAGGGAA GGCTCTGCC	2884
TGGCCTTCCG TCAGCTCTGC CAGTGCAGGC TGGGCAGCCT GGGCTTCTAGA GCTGGCTTCT	2944
GCCCCACACTT TCTCCGTGAA AGGAAAACAA CTATGAGTCT GCCAAACGCA TCTCAGATGC	3004
GTTTTAAAAA ATTCTGGTCC CCGCTCTCTG TCCCACATCATC CGCCTGGGG ACTTCCTCTC	3064
TCCGTGGTTC TCACCCCCATA CTCTGTCACT GCCACATTT CACCTGGGCC TGGCCTTTGT	3124
CTCCACCTGA AACTCCTGAA AATCTTGAAA TGGATTCTA GGTCACTGGG GACTCCGGCA	3184
GCACATTGGG CTTCAGAATA AAGGGCGCCC GCGGTCCCCC AGCACCTCCC CAAGCCACAC	3244
CCCTAGCTTC CCTCCCTATC CCTGCAGCCT GAGGGTCCCT TCAGCCACCC TTAAGTCCCC	3304
ACCTGGGCTC CTGCCCCGCC CCTGGCTAGC AGCGCCTTCT CCACCGGGGC CCCCTCTGCT	3364
CACAGAGCCC CCTCACCTCC CTGGGGATGA GGGGCCAGGC CATGACCTG AAAGTCTAGC	3424
CCTGGCCTTG ACCTCCCAGG AGCGCCCTCC CCGCCCTCTC CGGGCCCCGG CCCCGTCC	3484
TGCTGCTGGC CTCTGGGTG TGCCCCGAG ACTGAGCTGC GCTTGGGGGT CCTGGCGGCC	3544
TGGGCCGTCC CGCACCGAAC CCAGGGCGTC GGAGGCCGGC GGGAGGGCGC GAGGTCC	3604
TGGGGGCTCC TCCGACGCCCT GAGGGCGCTG CTTCCCCGCG GCGCCCCCGG GTTCTGC	3664

AGCCGGGGCC	TCCGCTCTG	GGTGACCCGG	TGAGACCCCC	GGGGAGGCCG	CTGGGGAGGC	3724
GCGGGCTCTG	CTCCCCGGTC	CCAAACGCAC	TGGCTGCC	TCAGGAGGGA	CGGCGACCTC	3784
CACCCACGGC	GCTGGCGCCC	GCACGGCCGC	TCCTCCCGCT	CCCGCAGCCT	GGACGCCTCC	3844
CGAGGCCGCC	CCGCCGGGCC	CCACGCGGG	CCCCATCCGC	AGGCCAGGAC	TGCCTTCCCG	3904
GAGCTGGCGG	CCCCCAGCCT	GGAGGAGCCG	GCCCCAGACG	CCCTCCCAGC	CCTCCCCAGC	3964
CCACTCTGGC	CCCGCAGCCC	CCGCCTGGTC	CGAGTGCAGG	TCTCTGCC	CGGCCTTCC	4024
CGGGGAAGGA	AAGCAAAAG	CTT				4047

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Met	Asn	Gly	Asp	Met	Pro	His	Val	Pro	Ile	Thr	Thr	Leu	Ala	Gly	Ile
1				5					10						15
Ala	Ser	Leu	Thr	Asp	Leu	Leu	Asn	Gln	Leu	Pro	Leu	Pro	Ser	Pro	Leu
					20				25						30
Pro	Ala	Thr	Thr	Thr	Lys	Ser	Leu	Leu	Phe	Asn	Ala	Arg	Ile	Ala	Glu
					35				40			45			
Glu	Val	Asn	Cys	Leu	Leu	Ala	Cys	Arg	Asp	Asp	Asn	Leu	Val	Ser	Gln
					50				55			60			
Leu	Val	His	Ser	Leu	Asn	Gln	Val	Ser	Thr	Asp	His	Ile	Glu	Leu	Lys
					65				70			75			80
Asp	Asn	Leu	Gly	Ser	Asp	Asp	Pro	Glu	Gly	Asp	Ile	Pro	Val	Leu	Leu
					85				90			95			
Gln	Ala	Val	Leu	Ala	Arg	Ser	Pro	Asn	Val	Phe	Arg	Glu	Ser	Met	
					100				105			110			
Gln	Asn	Arg	Tyr	Val	Gln	Ser	Gly	Met	Met	Met	Ser	Gln	Tyr	Lys	Leu
					115				120			125			
Ser	Gln	Asn	Ser	Met	His	Ser	Ser	Pro	Ala	Ser	Ser	Asn	Tyr	Gln	Gln
					130				135			140			
Thr	Thr	Ile	Ser	His	Ser	Pro	Ser	Ser	Arg	Phe	Val	Pro	Pro	Gln	Thr
					145				150			155			160
Ser	Ser	Gly	Asn	Arg	Phe	Met	Pro	Gln	Gln	Asn	Ser	Pro	Val	Pro	Ser
					165				170			175			
Pro	Tyr	Ala	Pro	Gln	Ser	Pro	Ala	Gly	Tyr	Met	Pro	Tyr	Ser	His	Pro
					180				185			190			
Ser	Ser	Tyr	Thr	Thr	His	Pro	Gln	Met	Gln	Gln	Ala	Ser	Val	Ser	Ser
					195				200			205			
Pro	Ile	Val	Ala	Gly	Gly	Leu	Arg	Asn	Ile	His	Asp	Asn	Lys	Val	Ser
					210				215			220			
Gly	Pro	Leu	Ser	Gly	Asn	Ser	Ala	Asn	His	His	Ala	Asp	Asn	Pro	Arg
					225				230			235			240
His	Gly	Ser	Ser	Glu	Asp	Tyr	Leu	His	Met	Val	His	Arg	Leu	Ser	Ser
					245				250			255			
Asp	Asp	Gly	Asp	Ser	Ser	Thr	Met	Arg	Asn	Ala	Ala	Ser	Phe	Pro	Leu
					260				265			270			
Arg	Ser	Pro	Gln	Pro	Val	Cys	Ser	Pro	Ala	Gly	Ser	Glu	Gly	Thr	Pro
					275				280			285			

Lys Gly Ser Arg Pro Pro Leu Ile Leu Gln Ser Gln Ser Leu Pro Cys
 290 295 300
 Ser Ser Pro Arg Asp Val Pro Pro Asp Ile Leu Leu Asp Ser Pro Glu
 305 310 315 320
 Arg Lys Gln Lys Lys Gln Lys Lys Met Lys Leu Gly Lys Asp Glu Lys
 325 330 335
 Glu Gln Ser Glu Lys Ala Ala Met Tyr Asp Ile Ile Ser Ser Pro Ser
 340 345 350
 Lys Asp Ser Thr Lys Leu Thr Leu Arg Leu Ser Arg Val Arg Ser Ser
 355 360 365
 Asp Met Asp Gln Gln Glu Asp Met Ile Ser Gly Val Glu Asn Ser Asn
 370 375 380
 Val Ser Glu Asn Asp Ile Pro Phe Asn Val Gln Tyr Pro Gly Gln Thr
 385 390 395 400
 Ser Lys Thr Pro Ile Thr Pro Gln Asp Ile Asn Arg Pro Leu Asn Ala
 405 410 415
 Ala Gln Cys Leu Ser Gln Gln Glu Gln Thr Ala Phe Leu Pro Ala Asn
 420 425 430
 Gln Val Pro Val Leu Gln Gln Asn Thr Ser Val Ala Ala Lys Gln Pro
 435 440 445
 Gln Thr Asn Ser His Lys Thr Leu Val Gln Pro Gly Thr Gly Ile Glu
 450 455 460
 Val Ser Ala Glu Leu Pro Lys Asp Lys Thr
 465 470

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence

- (B) LOCATION: 26...799

- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

- AAGCTTTTG AATTGGCAC GAGAT GCT ACA CAG GCT ATA TTT GAA ATA CTG	52
Ala Thr Gln Ala Ile Phe Glu Ile Leu	
1 5	
GAG AAA TCC TGG TTG CCC CAG AAT TGT ACA CTG GTT GAT ATG AAG ATT	100
Glu Lys Ser Trp Leu Pro Gln Asn Cys Thr Leu Val Asp Met Lys Ile	
10 15 20 25	
GAA TTT GGT GTT GAT GTA ACC ACC AAA GAA ATT GTT CTT GCT GAT GTT	148
Glu Phe Gly Val Asp Val Thr Thr Lys Glu Ile Val Leu Ala Asp Val	
30 35 40	
ATT GAC AAT GAT TCC TGG AGA CTC TGG CCA TCA GGA GAT CGA AGC CAA	196
Ile Asp Asn Asp Ser Trp Arg Leu Trp Pro Ser Gly Asp Arg Ser Gln	
45 50 55	

CAG AAA GAC AAA CAG TCT TAT CGG GAC CTC AAA GAA GTA ACT CCT GAA		244	
Gln Lys Asp Lys Gln Ser Tyr Arg Asp Leu Lys Glu Val Thr Pro Glu			
60	65	70	
GGG CTC CAA ATG GTA AAG AAA AAC TTT GAG TGG GTT GCA GAG AGA GTA		292	
Gly Leu Gln Met Val Lys Lys Asn Phe Glu Trp Val Ala Glu Arg Val			
75	80	85	
GAG TTG CTT TTG AAA TCA GAA AGT CAG TGC AGG GTT GTA GTG TTG ATG		340	
Glu Leu Leu Leu Lys Ser Glu Ser Gln Cys Arg Val Val Val Leu Met			
90	95	100	105
GGC TCT ACT TCT GAT CTT GGT CAC TGT GAA AAA ATC AAG AAG GCC TGT		388	
Gly Ser Thr Ser Asp Leu Gly His Cys Glu Lys Ile Lys Lys Ala Cys			
110	115	120	
GGA AAT TTT GGC ATT CCA TGT GAA CTT CGA GTA ACA TCT GCG CAT AAA		436	
Gly Asn Phe Gly Ile Pro Cys Glu Leu Arg Val Thr Ser Ala His Lys			
125	130	135	
GGA CCA GAT GAA ACT CTG AGG ATT AAA GCT GAG TAT GAA GGG GAT GGC		484	
Gly Pro Asp Glu Thr Leu Arg Ile Lys Ala Glu Tyr Glu Gly Asp Gly			
140	145	150	
ATT CCT ACT GTA TTT GTG GCA GTG GCA GGC AGA AGT AAT GGT TTG GGA		532	
Ile Pro Thr Val Phe Val Ala Val Ala Gly Arg Ser Asn Gly Leu Gly			
155	160	165	
CCA GTG ATG TCT GGG AAC ACT GCA TAT CCA GTT ATC AGC TGT CCT CCC		580	
Pro Val Met Ser Gly Asn Thr Ala Tyr Pro Val Ile Ser Cys Pro Pro			
170	175	180	185
CTC ACA CCA GAC TGG GGA GTT CAG GAT GTG TGG TCT TCT CTT CGA CTA		628	
Leu Thr Pro Asp Trp Gly Val Gln Asp Val Trp Ser Ser Leu Arg Leu			
190	195	200	
CCC AGT GGT CTT GGC TGT TCA ACC GTA CTT TCT CCA GAA GGA TCA GCT		676	
Pro Ser Gly Leu Gly Cys Ser Thr Val Leu Ser Pro Glu Gly Ser Ala			
205	210	215	
CAA TTT GCT GCT CAG ATA TTT GGG TTA AGC AAC CAT TTG GTA TGG AGC		724	
Gln Phe Ala Ala Gln Ile Phe Gly Leu Ser Asn His Leu Val Trp Ser			
220	225	230	
AAA CTG CGA GCA AGC ATT TTG AAC ACA TGG ATT TCC TTG AAG CAG GCT		772	
Lys Leu Arg Ala Ser Ile Leu Asn Thr Trp Ile Ser Leu Lys Gln Ala			
235	240	245	
GAC AAG AAA ATC AGA GAA TGT AAT TTA TAAGAAAGAA TGCCATTGAA TTTTTA		826	
Asp Lys Lys Ile Arg Glu Cys Asn Leu			
250	255		
GGGGAAAAAC TACAAATTTC TAATTTAGCT GAAGGAAAAT CAAGCAAGAT GAAAAGGTAA		886	
TTTTAAATTA GAGAACACAA ATAAAATGTA TTAGTGAATA AATGGTGAGG GTAGGCCTAT		946	
TCAGATGCAA GGCCAGCAAT GGGGCTCCCC ATTATCCCCA CCCCTTGGT CCCAGTCCCC		1006	
TTCTCTGCAA TGGGCACGCA TAGAGGAGAG ACAAAAGGGTA TTAGACGCAA CATCATTGGC		1066	

CCAGGGGAGT	CCGAGAAGAG	CTGCCATTGG	CTGACAGGGC	ATTTCAGGC	TCTGTCATTG	1126
GTCAGGGAGC	ACACCCCAGC	CTGAAGAGTG	ATGCCATTGG	CCAGGGAGTG	GTTTGTCTAT	1186
AGCCGTTGGC	TGTGAAGTGG	AAGGAAAAGA	TCTGGGAATG	AAGCCCTGTG	GCCAGGAAGA	1246
TAGACAGGGC	AGCAACTTCT	GGGCCTCCAG	GCCCTCTTCC	CACCATAGCA	ATGTGGGCAA	1306
AACTGGTGTG	AGGCCCCAGC	CAGAAAAAAGG	AGCCAAGCC	AGAGGGCAAG	TGACAAAGGA	1366
TGTACCATGT	CCAATCTCCC	ACACCCCTGGG	GCTGCCCTTC	CCAATGTCTT	TCTGATAGC	1426
CAAGTTGGGC	TGGGAGCAGC	TCACTGCTCC	TCTAGCCAGG	AGGGTTTCTC	AGCTCCTGGA	1486
GGCCGCAGCT	TGATGTTGAA	CTGCTGCAGG	GTCTGCTCCA	GCTGTTCTG	GTTCCCAGCA	1546
AAGTAGGGCGG	ACACAGCATT	GTGGAAGAGC	AGCAGCTGCT	TGTGCATCAC	CTTGATCTTG	1606
TTTCTTCCA	GGAACCTGAG	CTTGATGGCC	ACATCTCCCC	GCAGCTTCTC	ATACTTGTCC	1666
CGATGGGCCT	GGAAAGTGGC	CTGGGCACTC	TCAAGTCGAC	CACGTGTC	TGCATCCCAGG	1726
GGGCCTAGAC	TCAGCTCCTC	TAAGTCTGTT	CGGTAGGCAT	CATATTCCAG	CCTGGCAGCC	1786
TCATACTGTT	TCACAGTCAT	GAGCGTGTCT	TCCATGGTCT	TGGTGACCAA	TGTGTTGATG	1846
CTAGAGACAA	AGAAGTCAC	GGCTCCTAGC	AGCGTTCCC	CATTCTTGCA	TAGTAGTTTC	1906
TGTGTCTCTG	CATTGAGGCC	AAATTCCCTCC	TGAAGCTCTG	GGGACTTCTG	GCTGAGGTCA	1966
GCAAAGGCAT	CACCCAGTGC	ATGCTGGGTC	TGCAGCAGGC	TGTAGAGGTG	GGCTGTCAGT	2026
GCCCAGGCCA	GCTGCAGGAC	ACTCTCATAC	TTGCGCTTCG	TCTCACCGCAG	CAACTCAATC	2086
TGCAGCTCTA	GCTCCAGGAT	TCCGGCGCCT	CCACTCCGTC	CCCCGCGGGT	CTGCTCTGTG	2146
TGCCATGGAC	GGCATTGTCC	CAGATATAGC	CGTTGGTACA	AAGCGGGGAT	CTGACGAGCT	2206
TTTCTCTACT	TGTGTCACTA	ACGGACCGTT	TATCATGAGC	AGCAACTCGG	CTTCTGCAGC	2266
AAACGGAAAT	GACAGCAAGA	AGTTCAAAGG	TGACAGCCGA	AGTGCAGGCG	TCCCCCTCTAG	2326
AGTGATCCAC	ATCCGGAAGC	TCCCCATCGA	CGTCACGGAG	GGGGAAGTCA	TCTCCCTGGG	2386
GCTGCCCTTT	GGGAAGGTCA	CCAACCTCCT	GATGCTGAAG	GGGAAAACC	AGGCCTTCAT	2446
CGAGATGAAC	ACGGAGGAGG	CTGCCAATAC	CATGGTGAAC	TACTACACCT	CGGTGACCCC	2506
TGTGCTGCGC	GGCCAGGCCA	TCTACATCCA	GTTCCTCAAC	CACAAGGAGC	TGAAGACCGA	2566
CAGCTCTCCC	AACCAGGCAGC	GGGCCCAGGC	GGCCCTGCGAG	GCGGTGAAC	CGGTCCAGTC	2626
GGGGAACCTG	GCCTTGGCTG	CCTCGGCGGC	GGCGTGGAT	GCAGGGATGG	CGATGGCCGG	2686
GCAGAGCCCC	GTGCTCAGGA	TCATCGTGGA	GAACCTCTTC	TACCCCTGTGA	CCCTGGATGT	2746
GCTGCACCAG	ATTTCTCCA	AGTTCCGGCAC	AGTGGTGAAG	ATCATCACCT	TCACCAAGAA	2806
CAACCAGTTC	CAGGCCCTGC	TGCAGTATGC	GGACCCCGTG	AGCGCCCAGC	ACGCCAAGCT	2866
GTCGCTGGAC	GGGCAGAACAA	TCTACAACGC	CTGCTGCACG	CTGCGCATCG	ACTTTCCAA	2926
GCTCACCAAGC	CTAACACGTCA	AGTACAACAA	TGACAAGAGC	CGTGACTACC	TCGTGCCGAA	2986
TTCTTGGAT	CC					2998

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Ala	Thr	Gln	Ala	Ile	Phe	Glu	Ile	Leu	Glu	Lys	Ser	Trp	Leu	Pro	Gln
1				5				10					15		
Asn	Cys	Thr	Leu	Val	Asp	Met	Lys	Ile	Glu	Phe	Gly	Val	Asp	Val	Thr
						20			25				30		
Thr	Lys	Glu	Ile	Val	Leu	Ala	Asp	Val	Ile	Asp	Asn	Asp	Ser	Trp	Arg
						35			40				45		
Leu	Trp	Pro	Ser	Gly	Asp	Arg	Ser	Gln	Gln	Lys	Asp	Lys	Gln	Ser	Tyr
						50			55				60		
Arg	Asp	Leu	Lys	Glu	Val	Thr	Pro	Glu	Gly	Leu	Gln	Met	Val	Lys	Lys
						65			70				75		80

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1038 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

```

Ile Gln Arg Phe Gly Thr Ser Gly His Ile Met Asn Leu Gln Ala Gln
      1           5           10          15
Pro Lys Ala Gln Asn Lys Arg Lys Arg Cys Leu Phe Gly Gly Gln Glu
      20          25          30
Pro Ala Pro Lys Glu Gln Pro Pro Pro Leu Gln Pro Pro Gln Gln Ser
      35          40          45
- Ile Arg Val Lys Glu Glu Gln Tyr Leu Gly His Glu Gly Pro Gly Gly
      50          55          60
Ala Val Ser Thr Ser Gln Pro Val Glu Leu Pro Pro Pro Ser Ser Leu
      65          70          75          80
Ala Leu Leu Asn Ser Val Val Tyr Gly Pro Glu Arg Thr Ser Ala Ala
      85          90          95
Met Leu Ser Gln Gln Val Ala Ser Val Lys Trp Pro Asn Ser Val Met
      100         105         110
Ala Pro Gly Arg Gly Pro Glu Arg Gly Gly Gly Gly Val Ser Asp
      115         120         125
Ser Ser Trp Gln Gln Gln Pro Gly Gln Pro Pro Pro His Ser Thr Trp
      130         135         140
Asn Cys His Ser Leu Ser Leu Tyr Ser Ala Thr Lys Gly Ser Pro His
      145         150         155         160
Pro Gly Val Gly Val Pro Thr Tyr Tyr Asn His Pro Glu Ala Leu Lys

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165	170	175	
Arg Glu Lys Ala Gly Gly Pro Gln Leu Asp Arg Tyr Val Arg Pro Met			
180	185	190	
Met Pro Gln Lys Val Gln Leu Glu Val Gly Arg Pro Gln Ala Pro Leu			
195	200	205	
Asn Ser Phe His Ala Ala Lys Lys Pro Pro Asn Gln Ser Leu Pro Leu			
210	215	220	
Gln Pro Phe Gln Leu Ala Phe Gly His Gln Val Asn Arg Gln Val Phe			
225	230	235	240
Arg Gln Gly Pro Pro Pro Asn Pro Val Ala Ala Phe Pro Pro Gln			
245	250	255	
Lys Gln Gln Gln Gln Gln Pro Gln Gln Gln Gln Gln Gln Gln Gln			
260	265	270	
Ala Ala Leu Pro Gln Met Pro Leu Phe Glu Asn Phe Tyr Ser Met Pro			
275	280	285	
Gln Gln Pro Ser Gln Gln Pro Gln Asp Phe Gly Leu Gln Pro Ala Gly			
290	295	300	
Pro Leu Gly Gln Ser His Leu Ala His His Ser Met Ala Pro Tyr Pro			
305	310	315	320
Phe Pro Pro Asn Pro Asp Met Asn Pro Glu Leu Arg Lys Ala Leu Leu			
325	330	335	
Gln Asp Ser Ala Pro Gln Pro Ala Leu Pro Gln Val Gln Ile Pro Phe			
340	345	350	
Pro Arg Arg Ser Arg Arg Leu Ser Lys Glu Gly Ile Leu Pro Pro Ser			
355	360	365	
Ala Leu Asp Gly Ala Gly Thr Gln Pro Gly Gln Glu Ala Thr Gly Asn			
370	375	380	
Leu Phe Leu His His Trp Pro Leu Gln Gln Pro Pro Pro Gly Ser Leu			
385	390	395	400
Gly Gln Pro His Pro Glu Ala Leu Gly Phe Pro Leu Glu Leu Arg Glu			
405	410	415	
Ser Gln Leu Leu Pro Asp Gly Glu Arg Leu Ala Pro Asn Gly Arg Glu			
420	425	430	
Arg Glu Ala Pro Ala Met Gly Ser Glu Glu Gly Met Arg Ala Val Ser			
435	440	445	
Thr Gly Asp Cys Gly Gln Val Leu Arg Gly Gly Val Ile Gln Ser Thr			
450	455	460	
Arg Arg Arg Arg Ala Ser Gln Glu Ala Asn Leu Leu Thr Leu Ala			
465	470	475	480
Gln Lys Ala Val Glu Leu Ala Ser Leu Gln Asn Ala Lys Asp Gly Ser			
485	490	495	
Gly Ser Glu Glu Lys Arg Lys Ser Val Leu Ala Ser Thr Thr Lys Cys			
500	505	510	
Gly Val Glu Phe Ser Glu Pro Ser Leu Ala Thr Lys Arg Ala Arg Glu			
515	520	525	
Asp Ser Gly Met Val Pro Leu Ile Ile Pro Val Ser Val Pro Val Arg			
530	535	540	
Thr Val Asp Pro Thr Glu Ala Ala Gln Ala Gly Leu Asp Glu Asp			
545	550	555	560
Gly Lys Gly Leu Glu Gln Asn Pro Ala Glu His Lys Pro Ser Val Ile			
565	570	575	
Val Thr Arg Arg Ser Thr Arg Ile Pro Gly Thr Asp Ala Gln Ala			
580	585	590	
Gln Ala Glu Asp Met Asn Val Lys Leu Glu Gly Glu Pro Ser Val Arg			
595	600	605	
Lys Pro Lys Gln Arg Pro Arg Pro Glu Pro Leu Ile Ile Pro Thr Lys			
610	615	620	

Ala Gly Thr Phe Ile Ala Pro Pro Val Tyr Ser Asn Ile Thr Pro Tyr
 625 630 635 640
 Gln Ser His Leu Arg Ser Pro Val Arg Leu Ala Asp His Pro Ser Glu
 645 650 655
 Arg Ser Phe Glu Leu Pro Pro Tyr Thr Pro Pro Pro Ile Leu Ser Pro
 660 665 670
 Val Arg Glu Gly Ser Gly Leu Tyr Phe Asn Ala Ile Ile Ser Thr Ser
 675 680 685
 Thr Ile Pro Ala Pro Pro Ile Thr Pro Lys Ser Ala His Arg Thr
 690 695 700
 Leu Leu Arg Thr Asn Ser Ala Glu Val Thr Pro Pro Val Leu Ser Val
 705 710 715 720
 Met Gly Glu Ala Thr Pro Val Ser Ile Glu Pro Arg Ile Asn Val Gly
 725 730 735
 Ser Arg Phe Gln Ala Glu Ile Pro Leu Met Arg Asp Arg Ala Leu Ala
 740 745 750
 Ala Ala Asp Pro His Lys Ala Asp Leu Val Trp Gln Pro Trp Glu Asp
 755 760 765
 Leu Glu Ser Ser Arg Glu Lys Gln Arg Gln Val Glu Asp Leu Leu Thr
 770 775 780
 Ala Ala Cys Ser Ser Ile Phe Pro Gly Ala Gly Thr Asn Gln Glu Leu
 785 790 795 800
 Ala Leu His Cys Leu His Glu Ser Arg Gly Asp Ile Leu Glu Thr Leu
 805 810 815
 Asn Lys Leu Leu Leu Lys Lys Pro Leu Arg Pro His Asn His Pro Leu
 820 825 830
 Ala Thr Tyr His Tyr Thr Gly Ser Asp Gln Trp Lys Met Ala Glu Arg
 835 840 845
 Lys Leu Phe Asn Lys Gly Ile Ala Ile Tyr Lys Lys Asp Phe Phe Leu
 850 855 860
 Val Gln Lys Leu Ile Gln Thr Lys Thr Val Ala Gln Cys Val Glu Phe
 865 870 875 880
 Tyr Tyr Thr Tyr Lys Lys Gln Val Lys Ile Gly Arg Asn Gly Thr Leu
 885 890 895
 Thr Phe Gly Asp Val Asp Thr Ser Asp Glu Lys Ser Ala Gln Glu Glu
 900 905 910
 Val Glu Val Asp Ile Lys Thr Ser Gln Lys Phe Pro Arg Val Pro Leu
 915 920 925
 Pro Arg Arg Glu Ser Pro Ser Glu Glu Arg Leu Glu Pro Lys Arg Glu
 930 935 940
 Val Lys Glu Pro Arg Lys Glu Gly Glu Glu Val Pro Glu Ile Gln
 945 950 955 960
 - Glu Lys Glu Glu Gln Glu Glu Gly Arg Glu Arg Ser Arg Arg Ala Ala
 965 970 975
 Ala Val Lys Ala Thr Gln Thr Leu Gln Ala Asn Glu Ser Ala Ser Asp
 980 985 990
 Ile Leu Ile Leu Arg Ser His Glu Ser Asn Ala Pro Gly Ser Ala Gly
 995 1000 1005
 Gly Gln Ala Ser Glu Lys Pro Arg Glu Gly Thr Gly Lys Ser Arg Arg
 1010 1015 1020
 Ala Leu Pro Phe Ser Glu Lys Lys Lys Lys Gln Lys Ala
 1025 1030 1035

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 849 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Ile Arg His Glu Val Ser Phe Leu Trp Asn Thr Glu Ala Ala Cys Pro
1 5 10 15
Ile Gln Thr Thr Asp Thr Asp Gln Ala Cys Ser Ile Arg Asp Pro
20 25 30
Asn Ser Gly Phe Val Phe Asn Leu Asn Pro Leu Asn Ser Ser Gln Gly
35 40 45
Tyr Asn Val Ser Gly Ile Gly Lys Ile Phe Met Phe Asn Val Cys Gly
50 55 60
Thr Met Pro Val Cys Gly Thr Ile Leu Gly Lys Pro Ala Ser Gly Cys
65 70 75 80
Glu Ala Glu Thr Gln Thr Glu Glu Leu Lys Asn Trp Lys Pro Ala Arg
85 90 95
Pro Val Gly Ile Glu Lys Ser Leu Gln Leu Ser Thr Glu Gly Phe Ile
100 105 110
Thr Leu Thr Tyr Lys Gly Pro Leu Ser Ala Lys Gly Thr Ala Asp Ala
115 120 125
Phe Ile Val Arg Phe Val Cys Asn Asp Asp Val Tyr Ser Gly Pro Leu
130 135 140
Lys Phe Leu His Gln Asp Ile Asp Ser Gly Gln Gly Ile Arg Asn Thr
145 150 155 160
Tyr Phe Glu Phe Glu Thr Ala Leu Ala Cys Val Pro Ser Pro Val Asp
165 170 175
Cys Gln Val Thr Asp Leu Ala Gly Asn Glu Tyr Asp Leu Thr Gly Leu
180 185 190
Ser Thr Val Arg Lys Pro Trp Thr Ala Val Asp Thr Ser Val Asp Gly
195 200 205
Arg Lys Arg Thr Phe Tyr Leu Ser Val Cys Asn Pro Leu Pro Tyr Ile
210 215 220
Pro Gly Cys Gln Gly Ser Ala Val Gly Ser Cys Leu Val Ser Glu Gly
225 230 235 240
Asn Ser Trp Asn Leu Gly Val Val Gln Met Ser Pro Gln Ala Ala Ala
245 250 255
Asn Gly Ser Leu Ser Ile Met Tyr Val Asn Gly Asp Lys Cys Gly Asn
260 265 270
Gln Arg Phe Ser Thr Arg Ile Thr Phe Glu Cys Ala Gln Ile Ser Gly
275 280 285
Ser Pro Ala Phe Gln Leu Gln Asp Gly Cys Glu Tyr Val Phe Ile Trp
290 295 300
Arg Thr Val Glu Ala Cys Pro Val Val Arg Val Glu Gly Asp Asn Cys
305 310 315 320
Glu Val Lys Asp Pro Arg His Gly Asn Leu Tyr Asp Leu Lys Pro Leu
325 330 335
Gly Leu Asn Asp Thr Ile Val Ser Ala Gly Glu Tyr Thr Tyr Tyr Phe
340 345 350
Arg Val Cys Gly Lys Leu Ser Ser Asp Val Cys Pro Thr Ser Asp Lys
355 360 365
Ser Lys Val Val Ser Ser Cys Gln Glu Lys Arg Glu Pro Gln Gly Phe
370 375 380
His Lys Val Ala Gly Leu Leu Thr Gln Lys Leu Thr Tyr Glu Asn Gly
385 390 395 400

Leu Leu Lys Met Asn Phe Thr Gly Gly Asp Thr Cys His Lys Val Tyr
 405 410 415
 Gln Arg Ser Thr Ala Ile Phe Phe Tyr Cys Asp Arg Gly Thr Gln Arg
 420 425 430
 Pro Val Phe Leu Lys Glu Thr Ser Asp Cys Ser Tyr Leu Phe Glu Trp
 435 440 445
 Arg Thr Gln Tyr Ala Cys Pro Pro Phe Asp Leu Thr Glu Cys Ser Phe
 450 455 460
 Lys Asp Gly Ala Gly Asn Ser Phe Asp Leu Ser Ser Leu Ser Arg Tyr
 465 470 475 480
 Ser Asp Asn Trp Glu Ala Ile Thr Gly Thr Gly Asp Pro Glu His Tyr
 485 490 495
 Leu Ile Asn Val Cys Lys Ser Leu Ala Pro Gln Ala Gly Thr Glu Pro
 500 505 510
 Cys Pro Pro Glu Ala Ala Ala Cys Leu Leu Gly Gly Ser Lys Pro Val
 515 520 525
 Asn Leu Gly Arg Val Arg Asp Gly Pro Gln Trp Arg Asp Gly Ile Ile
 530 535 540
 Val Leu Lys Tyr Val Asp Gly Asp Leu Cys Pro Asp Gly Ile Arg Lys
 545 550 555 560
 Lys Ser Thr Thr Ile Arg Phe Thr Cys Ser Glu Ser Gln Val Asn Ser
 565 570 575
 Arg Pro Met Phe Ile Ser Ala Val Glu Asp Cys Glu Tyr Thr Phe Ala
 580 585 590
 Trp Pro Thr Ala Thr Ala Cys Pro Met Lys Ser Asn Glu His Asp Asp
 595 600 605
 Cys Gln Val Thr Asn Pro Ser Thr Gly His Leu Phe Asp Leu Ser Ser
 610 615 620
 Leu Ser Gly Arg Ala Gly Phe Thr Ala Ala Tyr Ser Glu Lys Gly Leu
 625 630 635 640
 Val Tyr Met Ser Ile Cys Gly Glu Asn Glu Asn Cys Pro Pro Gly Val
 645 650 655
 Gly Ala Cys Phe Gly Gln Thr Arg Ile Ser Val Gly Lys Ala Asn Lys
 660 665 670
 Arg Leu Arg Tyr Val Asp Gln Val Leu Gln Leu Val Tyr Lys Asp Gly
 675 680 685
 Ser Pro Cys Pro Ser Lys Ser Gly Leu Ser Tyr Lys Ser Val Ile Ser
 690 695 700
 Phe Val Cys Arg Pro Glu Ala Gly Pro Thr Asn Arg Pro Met Leu Ile
 705 710 715 720
 Ser Leu Asp Lys Gln Thr Cys Thr Leu Phe Phe Ser Trp His Thr Pro
 725 730 735
 - Leu Ala Cys Glu Gln Ala Thr Glu Cys Ser Val Arg Asn Gly Ser Ser
 740 745 750
 Ile Val Asp Leu Ser Pro Leu Ile His Arg Thr Gly Gly Tyr Glu Ala
 755 760 765
 Tyr Asp Glu Ser Glu Asp Asp Ala Ser Asp Thr Asn Pro Asp Phe Tyr
 770 775 780
 Ile Asn Ile Cys Gln Pro Leu Asn Pro Met His Gly Val Pro Cys Pro
 785 790 795 800
 Ala Gly Ala Ala Val Cys Lys Val Pro Ile Asp Gly Pro Pro Ile Asp
 805 810 815
 Ile Gly Arg Val Ala Gly Pro Pro Ile Leu Asn Pro Ile Ala Asn Glu
 820 825 830
 Ile Tyr Leu Asn Phe Glu Ser Ser Thr Pro Cys Gln Glu Phe Ser Cys
 835 840 845
 Lys

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Met Ala Arg Leu Ser Arg Pro Glu Arg Pro Asp Leu Val Phe Glu Glu
1 5 10 15
Glu Asp Leu Pro Tyr Glu Glu Glu Ile Met Arg Asn Gln Phe Ser Val
20 25 30
Lys Cys Trp Leu His Tyr Ile Glu Phe Lys Gln Gly Ala Pro Lys Pro
35 40 45
Arg Leu Asn Gln Leu Tyr Glu Arg Ala Leu Lys Leu Leu Pro Cys Ser
50 55 60
Tyr Lys Leu Trp Tyr Arg Tyr Leu Lys Ala Arg Arg Ala Gln Val Lys
65 70 75 80
His Arg Cys Val Thr Asp Pro Ala Tyr Glu Asp Val Asn Asn Cys His
85 90 95
Glu Arg Ala Phe Val Phe Met His Lys Met Pro Arg Leu Trp Leu Asp
100 105 110
Tyr Cys Gln Phe Leu Met Asp Gln Gly Arg Val Thr His Thr Arg Arg
115 120 125
Thr Phe Asp Arg Ala Leu Arg Ala Leu Pro Ile Thr Gln His Ser Arg
130 135 140
Ile Trp Pro Leu Tyr Leu Arg Phe Leu Arg Ser His Pro Leu Pro Glu
145 150 155 160
Thr Ala Val Arg Gly Tyr Arg Arg Phe Leu Lys Leu Ser Pro Glu Ser
165 170 175
Ala Glu Glu Tyr Ile Glu Tyr Leu Lys Ser Ser Asp Arg Leu Asp Glu
180 185 190
Ala Ala Gln Arg Leu Ala Thr Val Val Asn Asp Glu Arg Phe Val Ser
195 200 205
Lys Ala Gly Lys Ser Asn Tyr Gln Leu Trp His Glu Leu Cys Asp Leu
210 215 220
Ile Ser Gln Asn Pro Asp Lys Val Gln Ser Leu Asn Val Asp Ala Ile
225 230 235 240
Ile Arg Gly Gly Leu Thr Arg Phe Thr Asp Gln Leu Gly Lys Leu Trp
245 250 255
Cys Ser Leu Ala Asp Tyr Tyr Ile Arg Ser Gly His Phe Glu Lys Ala
260 265 270
Arg Asp Val Tyr Glu Glu Ala Ile Arg Thr Val Met Thr Val Arg Asp
275 280 285
Phe Thr Gln Val Phe Asp Ser Tyr Ala Gln Phe Glu Glu Ser Met Ile
290 295 300
Ala Ala Lys Met Glu Thr Ala Ser Glu Leu Gly Arg Glu Glu Glu Asp
305 310 315 320
Asp Val Asp Leu Glu Leu Arg Leu Ala Arg Phe Glu Gln Leu Ile Ser
325 330 335
Arg Arg Pro Leu Leu Asn Ser Val Leu Leu Arg Gln Asn Pro His
340 345 350

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D
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His Val His Glu Trp His Lys Arg Val Ala Leu His Gln Gly Arg Pro
355 360 365
Arg Glu Ile Ile Asn Thr Tyr Thr Glu Ala Val Gln Thr Val Asp Pro
370 375 380
Phe Lys Ala Thr Gly Lys Pro His Thr Leu Trp Val Ala Phe Ala Lys
385 390 395 400
Phe Tyr Glu Asp Asn Gly Gln Leu Asp Asp Ala Arg Val Ile Leu Glu
405 410 415
Lys Ala Thr Lys Val Asn Phe Lys Gln Val Asp Asp Leu Ala Ser Val
420 425 430
Trp Cys Gln Cys Gly Glu Leu Glu Leu Arg His Glu Asn Tyr Asp Glu
435 440 445
Ala Leu Arg Leu Leu Arg Lys Ala Thr Ala Leu Pro Ala Arg Arg Ala
450 455 460
Glu Tyr Phe Asp Gly Ser Glu Pro Val Gln Asn Arg Val Tyr Lys Ser
465 470 475 480
Leu Lys Val Trp Ser Met Leu Ala Asp Leu Glu Glu Ser Leu Gly Thr
485 490 495
Phe Gln Ser Thr Lys Ala Val Tyr Asp Arg Ile Leu Asp Leu Arg Ile
500 505 510
Ala Thr Pro Gln Ile Val Ile Asn Tyr Ala Met Phe Leu Glu Glu His
515 520 525
Lys Tyr Phe Glu Glu Ser Phe Lys Ala Tyr Glu Arg Gly Ile Ser Leu
530 535 540
Phe Lys Trp Pro Asn Val Ser Asp Ile Trp Ser Thr Tyr Leu Thr Lys
545 550 555 560
Phe Ile Ala Arg Tyr Gly Gly Arg Lys Leu Glu Arg Ala Arg Asp Leu
565 570 575
Phe Glu Gln Ala Leu Asp Gly Cys Pro Pro Lys Tyr Ala Lys Thr Leu
580 585 590
Tyr Leu Leu Tyr Ala Gln Leu Glu Glu Trp Gly Leu Ala Arg His
595 600 605
Ala Met Ala Val Tyr Glu Arg Ala Thr Arg Ala Val Glu Pro Ala Gln
610 615 620
Gln Tyr Asp Met Phe Asn Ile Tyr Ile Lys Arg Ala Ala Glu Ile Tyr
625 630 635 640
Gly Val Thr His Thr Arg Gly Ile Tyr Gln Lys Ala Ile Glu Val Leu
645 650 655
Ser Asp Glu His Ala Arg Glu Met Cys Leu Arg Phe Ala Asp Met Glu
660 665 670
Cys Lys Leu Gly Glu Ile Asp Arg Ala Arg Ala Ile Tyr Ser Phe Cys
675 680 685
Ser Gln Ile Cys Asp Pro Arg Thr Thr Gly Ala Phe Trp Gln Thr Trp
690 695 700
Lys Asp Phe Glu Val Arg His Gly Asn Glu Asp Thr Ile Lys Glu Met
705 710 715 720
Leu Arg Ile Arg Arg Ser Val Gln Ala Thr Tyr Asn Thr Gln Val Asn
725 730 735
Phe Met Ala Ser Gln Met Leu Lys Val Ser Gly Ser Ala Thr Gly Thr
740 745 750
Val Ser Asp Leu Ala Pro Gly Gln Ser Gly Met Asp Asp Met Lys Leu
755 760 765
Leu Glu Gln Arg Ala Glu Gln Leu Ala Ala Glu Ala Glu Arg Asp Gln
770 775 780
Pro Leu Arg Ala Gln Ser Lys Ile Leu Phe Val Arg Ser Asp Ala Ser
785 790 795 800
Arg Glu Glu Leu Ala Glu Leu Ala Gln Gln Val Asn Pro Glu Glu Ile

805	810	815
Gln Leu Gly Glu Asp Glu Asp Glu Asp	Glu Met Asp Leu Glu Pro Asn	
820	825	830
Glu Val Arg Leu Glu Gln Gln Ser Val Pro Ala Ala Val Phe Gly Ser		
835	840	845
Leu Lys Glu Asp		
850		

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Met Phe Ser Ala Leu Lys Leu Val Gly Ser Asp Gln Ala Pro Gly			
1	5	10	15
Arg Asp Lys Asn Ile Pro Ala Gly Leu Gln Ser Met Asn Gln Ala Leu			
20	25	30	
Gln Arg Arg Phe Ala Lys Gly Val Gln Tyr Asn Met Lys Ile Val Ile			
35	40	45	
Arg Gly Asp Arg Asn Thr Gly Lys Thr Ala Leu Trp His Arg Leu Gln			
50	55	60	
Gly Arg Pro Phe Val Glu Glu Tyr Ile Pro Thr Gln Glu Ile Gln Val			
65	70	75	80
Thr Ser Ile His Trp Ser Tyr Lys Thr Thr Asp Asp Ile Val Lys Val			
85	90	95	
Glu Val Trp Asp Val Val Asp Lys Gly Lys Cys Lys Lys Arg Gly Asp			
100	105	110	
Gly Leu Lys Met Glu Asn Asp Pro Gln Glu Xaa Glu Ser Glu Met Ala			
115	120	125	
Leu Asp Ala Glu Phe Leu Asp Val Tyr Lys Asn Cys Asn Gly Val Val			
130	135	140	
Met Met Phe Asp Ile Thr Lys Gln Trp Thr Phe Asn Tyr Ile Leu Arg			
145	150	155	160
Glu Leu Pro Lys Val Pro Thr His Val Pro Val Cys Val Leu Gly Asn			
165	170	175	
Tyr Arg Asp Met Gly Glu His Arg Val Ile Leu Pro Asp Asp Val Arg			
180	185	190	
Asp Phe Ile Asp Asn Leu Asp Arg Pro Pro Gly Ser Ser Tyr Phe Arg			
195	200	205	
Tyr Ala Glu Ser Ser Met Lys Asn Ser Phe Gly Leu Lys Tyr Leu His			
210	215	220	
Lys Phe Phe Asn Ile Pro Phe Leu Gln Leu Gln Arg Glu Thr Leu Leu			
225	230	235	240
Arg Gln Leu Glu Thr Asn Gln Leu Asp Met Asp Ala Thr Leu Glu Glu			
245	250	255	
Leu Ser Val Gln Gln Glu Thr Glu Asp Gln Asn Tyr Gly Ile Phe Leu			
260	265	270	
Glu Met Met Glu Ala Arg Ser Arg Gly His Ala Ser Pro Leu Ala Ala			
275	280	285	
Asn Gly Gln Ser Pro Ser Pro Gly Ser Gln Ser Pro Val Leu Pro Ala			
290	295	300	
Pro Ala Val Ser Thr Gly Ser Ser Ser Pro Gly Thr Pro Gln Pro Ala			

305	310	315	320
Pro Gln Leu Pro Leu Asn Ala Ala Pro Pro Ser Ser Val Pro Pro Val			
325	330	335	
Pro Pro Ser Glu Ala Leu Pro Pro Pro Ala Cys Pro Ser Ala Pro Ala			
340	345	350	
Pro Arg Arg Ser Ile Ile Ser Arg Leu Phe Gly Thr Ser Pro Ala Thr			
355	360	365	
Glu Ala Ala Pro Pro Pro Glu Pro Val Pro Ala Ala Gln Gly Pro			
370	375	380	
Ala Thr Val Gln Ser Val Glu Asp Phe Val Pro Asp Asp Arg Leu Asp			
385	390	395	400
Arg Ser Phe Leu Glu Asp Thr Thr Pro Ala Arg Asp Glu Lys Lys Val			
405	410	415	
Gly Ala Lys Ala Ala Gln Gln Asp Ser Asp Ser Asp Gly Glu Ala Leu			
420	425	430	
Gly Gly Asn Pro Met Val Ala Gly Phe Gln Asp Asp Val Asp Leu Glu			
435	440	445	
Asp Gln Pro Arg Gly Ser Pro Pro Leu Pro Ala Gly Pro Val Pro Ser			
450	455	460	
Gln Asp Ile Thr Leu Ser Ser Glu Glu Ala Glu Val Ala Ala Pro			
465	470	475	480
Thr Lys Gly Pro Ala Pro Ala Pro Gln Gln Cys Ser Glu Pro Glu Thr			
485	490	495	
Lys Trp Ser Ser Ile Pro Ala Ser Lys Pro Arg Arg Gly Thr Ala Pro			
500	505	510	
Thr Arg Thr Ala Ala Pro Pro Trp Pro Gly Gly Val Ser Val Arg Thr			
515	520	525	
Gly Pro Glu Lys Arg Ser Ser Thr Arg Pro Pro Ala Glu Met Glu Pro			
530	535	540	
Gly Lys Gly Glu Gln Ala Ser Ser Ser Glu Ser Asp Pro Glu Gly Pro			
545	550	555	560
Ile Ala Ala Gln Met Leu Ser Phe Val Met Asp Asp Pro Asp Phe Glu			
565	570	575	
Ser Glu Gly Ser Asp Thr Gln Arg Arg Ala Asp Asp Phe Pro Val Arg			
580	585	590	
Asp Asp Pro Ser Asp Val Thr Asp Glu Asp Glu Gly Pro Ala Glu Pro			
595	600	605	
Pro Pro Pro Pro Lys Leu Pro Leu Pro Ala Phe Arg Leu Lys Asn Asp			
610	615	620	
Ser Asp Leu Phe Gly Leu Gly Leu Glu Ala Gly Pro Lys Glu Ser			
625	630	635	640
Ser Glu Glu Gly Lys Glu Gly Lys Thr Pro Ser Lys Glu Lys Lys			
645	650	655	
Lys Thr Lys Ser Phe Ser Arg Val Leu Leu Glu Arg Pro Arg Ala His			
660	665	670	
Arg Phe Ser Thr Arg Val Gly Tyr Gln Val Ser Val Pro Asn Ser Pro			
675	680	685	
Tyr Ser Glu Ser Tyr			
690			